

Sequence Listing

- <110> Ashkenazi, Avi J.
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 Goddard, Audrey
 Godowski, Paul J.
 Grimaldi, J. Christopher
 Gurney, Austin L.
 Kljavin, Ivar J.
 Napier, Mary A.
 Pan, James
 Paoni, Nicholas F.
 Roy, Margaret Ann
 Stewart, Timothy A.
 Tumas, Daniel
 Watanabe, Colin K.
 Williams, P. Mickey
 Wood, William I.
 Zhang, Zemin
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tactccaatt atgttgacg tacactcatt gtacaggcgt ggagactcat 2650
tgtatgtata agaatatctc tgacagtgag tgaccggag tctctggtgt 2700
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tacaagtatt tagaactttt cagttcaggg caaatgttc atgaagttat 2800
tcctcttaaa catggttagg aagctgatga cgttattgat tttgtctgga 2850
ttatgtttct ggaataattt taccaaaaaca agctatttga gttttgactt 2900
gacaaggcaa aacatgacag tggattctct ttacaaatgg aaaaaaaaaa 2950
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tggtaaaaat tgtaaatata aatgtgcaac ttg 3033

<210> 6
<211> 251
<212> PRT
<213> Homo sapiens

<400> 6
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Arg Tyr Trp Phe Ala Ala Thr Val Ala Val Pro Leu Val Gly Lys
20 25 30
Leu Gly Leu Ile Ser Pro Ala Tyr Leu Phe Leu Trp Pro Glu Ala
35 40 45
Phe Leu Tyr Arg Phe Gln Ile Trp Arg Pro Ile Thr Ala Thr Phe
50 55 60
Tyr Phe Pro Val Gly Pro Gly Thr Gly Phe Leu Tyr Leu Val Asn
65 70 75
Leu Tyr Phe Leu Tyr Gln Tyr Ser Thr Arg Leu Glu Thr Gly Ala
80 85 90
Phe Asp Gly Arg Pro Ala Asp Tyr Leu Phe Met Leu Leu Phe Asn
95 100 105

Trp	Ile	Cys	Ile	Val	Ile	Thr	Gly	Leu	Ala	Met	Asp	Met	Gln	Leu
				110					115					120
Leu	Met	Ile	Pro	Leu	Ile	Met	Ser	Val	Leu	Tyr	Val	Trp	Ala	Gln
				125					130					135
Leu	Asn	Arg	Asp	Met	Ile	Val	Ser	Phe	Trp	Phe	Gly	Thr	Arg	Phe
				140					145					150
Lys	Ala	Cys	Tyr	Leu	Pro	Trp	Val	Ile	Leu	Gly	Phe	Asn	Tyr	Ile
				155					160					165
Ile	Gly	Gly	Ser	Val	Ile	Asn	Glu	Leu	Ile	Gly	Asn	Leu	Val	Gly
				170					175					180
His	Leu	Tyr	Phe	Phe	Leu	Met	Phe	Arg	Tyr	Pro	Met	Asp	Leu	Gly
				185					190					195
Gly	Arg	Asn	Phe	Leu	Ser	Thr	Pro	Gln	Phe	Leu	Tyr	Arg	Trp	Leu
				200					205					210
Pro	Ser	Arg	Arg	Gly	Gly	Val	Ser	Gly	Phe	Gly	Val	Pro	Pro	Ala
				215					220					225
Ser	Met	Arg	Arg	Ala	Ala	Asp	Gln	Asn	Gly	Gly	Gly	Gly	Arg	His
				230					235					240
Asn	Trp	Gly	Gln	Gly	Phe	Arg	Leu	Gly	Asp	Gln				
				245					250					

<210> 7
 <211> 1373
 <212> DNA
 <213> Homo sapiens

<400> 7
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 gtccggcggt ctggcctagg gatcttcccc gttgcccctt tggggcgagg 200
 tggctgcgga agaagaagac gaggtggagt gggtagtgga gagcatcgcg 250
 gggttcctgc gagggccaga ctggtccatc cccatcttgg actttgtgga 300
 acagaaatgt gaagttaact gcaaaggagg gcatgtgata actccaggaa 350
 gccagagacc ggtgattttg gtggcctgtg ttccccttgt ttttgatgat 400
 gaagaagaaa gcaaattgac ctatacagag attcatcagg aatacaaaga 450
 actagttgaa aagctgttag aaggttacct caaagaaatt ggaattaatg 500
 aagatcaatt tcaagaagca tgcacttctc ctcttgcaaa gaccataca 550
 tcacaggcca ttttgcaacc tgtgttgga gcagaagatt ttactatctt 600
 taaagcaatg atggtccaga aaaacattga aatgcagctg caagccattc 650
 gaataattca agagagaaat ggtgtattac ctgactgctt aaccgatggc 700

tctgatgtgg tcagtgacct tgaacacgaa gagatgaaaa tcctgagggg 750
 agttcttaga aaatcaaaaag aggaatatga ccaggaagaa gaaaggaaga 800
 ggaaaaaaca gttatcagag gctaaaacag aagagcccac agtgcattcc 850
 agtgaagctg caataatgaa taattcccaa ggggatgggtg aacattttgc 900
 acaccacccc tcagaagtta aaatgcattt tgctaatacag tcaatagaac 950
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 ggctgaaga ttcttggtt agagcatgag agcattgaag gaccaatagc 1050
 aaacttatca gtacttgga cagaagaact tcggcaacga gaacactatc 1100
 tcaagcagaa gagagataag ttgatgtcca tgagaaagga tatgaggact 1150
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 ggaaatgaca gagaaaccag aaatgacagc agaggagaag caaacattac 1250
 taaagaggag attgcttgca gagaaaactca aagaagaagt tattaataag 1300
 taataattaa gaacaattta acaaaatgga agttcaaatt gtcttaaaaa 1350
 taaattattt agtccttaca ctg 1373

<210> 8
 <211> 367
 <212> PRT
 <213> Homo sapiens

<400> 8
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 Ile Ala Gly Phe Leu Arg Gly Pro Asp Trp Ser Ile Pro Ile Leu
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 Asp Phe Val Glu Gln Lys Cys Glu Val Asn Cys Lys Gly Gly His
 35 40 45
 Val Ile Thr Pro Gly Ser Pro Glu Pro Val Ile Leu Val Ala Cys
 50 55 60
 Val Pro Leu Val Phe Asp Asp Glu Glu Glu Ser Lys Leu Thr Tyr
 65 70 75
 Thr Glu Ile His Gln Glu Tyr Lys Glu Leu Val Glu Lys Leu Leu
 80 85 90
 Glu Gly Tyr Leu Lys Glu Ile Gly Ile Asn Glu Asp Gln Phe Gln
 95 100 105
 Glu Ala Cys Thr Ser Pro Leu Ala Lys Thr His Thr Ser Gln Ala
 110 115 120
 Ile Leu Gln Pro Val Leu Ala Ala Glu Asp Phe Thr Ile Phe Lys
 125 130 135
 Ala Met Met Val Gln Lys Asn Ile Glu Met Gln Leu Gln Ala Ile
 140 145 150

Arg	Ile	Ile	Gln	Glu	Arg	Asn	Gly	Val	Leu	Pro	Asp	Cys	Leu	Thr
				155					160					165
Asp	Gly	Ser	Asp	Val	Val	Ser	Asp	Leu	Glu	His	Glu	Glu	Met	Lys
				170					175					180
Ile	Leu	Arg	Glu	Val	Leu	Arg	Lys	Ser	Lys	Glu	Glu	Tyr	Asp	Gln
				185					190					195
Glu	Glu	Glu	Arg	Lys	Arg	Lys	Lys	Gln	Leu	Ser	Glu	Ala	Lys	Thr
				200					205					210
Glu	Glu	Pro	Thr	Val	His	Ser	Ser	Glu	Ala	Ala	Ile	Met	Asn	Asn
				215					220					225
Ser	Gln	Gly	Asp	Gly	Glu	His	Phe	Ala	His	Pro	Pro	Ser	Glu	Val
				230					235					240
Lys	Met	His	Phe	Ala	Asn	Gln	Ser	Ile	Glu	Pro	Leu	Gly	Arg	Lys
				245					250					255
Val	Glu	Arg	Ser	Glu	Thr	Ser	Ser	Leu	Pro	Gln	Lys	Gly	Leu	Lys
				260					265					270
Ile	Pro	Gly	Leu	Glu	His	Ala	Ser	Ile	Glu	Gly	Pro	Ile	Ala	Asn
				275					280					285
Leu	Ser	Val	Leu	Gly	Thr	Glu	Glu	Leu	Arg	Gln	Arg	Glu	His	Tyr
				290					295					300
Leu	Lys	Gln	Lys	Arg	Asp	Lys	Leu	Met	Ser	Met	Arg	Lys	Asp	Met
				305					310					315
Arg	Thr	Lys	Gln	Ile	Gln	Asn	Met	Glu	Gln	Lys	Gly	Lys	Pro	Thr
				320					325					330
Gly	Glu	Val	Glu	Glu	Met	Thr	Glu	Lys	Pro	Glu	Met	Thr	Ala	Glu
				335					340					345
Glu	Lys	Gln	Thr	Leu	Leu	Lys	Arg	Arg	Leu	Leu	Ala	Glu	Lys	Leu
				350					355					360
Lys	Glu	Glu	Val	Ile	Asn	Lys								
				365										

<210> 9
 <211> 418
 <212> DNA
 <213> Homo sapiens

<400> 9
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 ctatacagag attcatcagg aatacaaaaga actagttgaa aagctgttag 100
 aaggttacct caaagaaatt ggaattaatg aagatcaatt tcaagaagca 150
 tgcacttctc ctcttgcaaa gaccataca tcacaggcca tttttgcaac 200
 ctgtgttggc agcagaagat ttactatct ttaaagcaat gatggtccag 250
 aaaaacattg aatgcagct gcaagccatt cgaataattc aagagagaaa 300

tggtgtatta cctgactgct taaccgatgg ctctgatgtg gtcagtgacc 350
 ttgaacacga agagatgaaa atcctgaggg aagttcttag aaaatcaaaa 400
 gaggaatatg accaggaa 418

<210> 10
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 10
 ttgacctata cagagattca tc 22

<210> 11
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 11
 ctaagaactt ccctcaggat ttt 23

<210> 12
 <211> 40
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 12
 atgaagatca atttcaagaa gcatgcactt ctctcttgc 40

<210> 13
 <211> 2886
 <212> DNA
 <213> Homo sapiens

<400> 13
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 ctatacctac tgtagcttct ccacgtatgg accctaaagg ctactgctgc 100
 tactacgggg ctagacagtt actgtctcag ctctaggatg tgcgttcttc 150
 cactagaagc tcttctgagg gaggtaatta aaaaacagtg gaatggaaaa 200
 acagtgtgt agtcctcctg taatatgctc cttgtcaaca atgtatacat 250
 tcttgctagg tgccatattc attgctttta gctcaagtcg catcttacta 300
 gtgaagtatt ctgccaatga agaaaacaag tatgattatc ttccaactac 350
 tgtgaatgtg tgctcagaac tggatgaagct agttttctgt gtgcttgtgt 400
 cattctgtgt tataaagaaa gatcatcaaa gtagaaattt gaaatatgct 450

tcoctggaagg aattctctga tttcatgaag tggccattc ctgcctttct 500
 ttattttcctg gataacttga ttgtcttcta tgtcctgtcc tatcttcaac 550
 cagccatggc tggtatcttc tcaaatttta gcattataac aacagctctt 600
 ctattcagga tagtgctgaa gaggcgtcta aactggatcc agtgggcttc 650
 cctcctgact ttatttttgt ctattgtggc cttgactgcc gggactaaaa 700
 ctttacagca caacttggca ggacgtggat ttcacacga tgcctttttc 750
 agcccttcca attcctgcct tcttttcaga agtgagtgtc ccagaaaaga 800
 caattgtaca gcaaaggaat ggacttttcc tgaagctaaa tggaacacca 850
 cagccagagt tttcagtcac atcctgtcttg gcattgggcca tgttcttatt 900
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 actgaaggag gggaaccagc tcaactgaaag catcttcata cagaacagca 1000
 aactctattt ctttggcatt ctgtttaatg ggcctgactc gggccttcag 1050
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 caggttacca ctgtcattat cacaacagtg totgtcctgg tctttgactt 1250
 caggccctcc ctggaatttt tcttgggaagc cccatcagtc cttctctcta 1300
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 ggatggagaa gaactagaaa gacttaccaa acccaagagt gatgagtcag 1450
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 tttgggatga tgtagtctgt gctaaatatt ttgctgaaga agcagtttct 2050

cagacacaac atctcagaat ttttaatTTTT agaaattcat gggaaattgg 2100
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 tctgctctcc tttctcctaa gtttcatgca gatgaatata aggtaatata 2800
 ctattatata attcatttTgt gatatccaca ataatatgac tggcaagaat 2850
 tgggtggaaat ttgtaattaa aataattatt aaacct 2886

<210> 14
 <211> 424
 <212> PRT
 <213> Homo sapiens

<400> 14
 Met Glu Lys Gln Cys Cys Ser His Pro Val Ile Cys Ser Leu Ser
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 Thr Met Tyr Thr Phe Leu Leu Gly Ala Ile Phe Ile Ala Leu Ser
 20 25 30
 Ser Ser Arg Ile Leu Leu Val Lys Tyr Ser Ala Asn Glu Glu Asn
 35 40 45
 Lys Tyr Asp Tyr Leu Pro Thr Thr Val Asn Val Cys Ser Glu Leu
 50 55 60
 Val Lys Leu Val Phe Cys Val Leu Val Ser Phe Cys Val Ile Lys
 65 70 75
 Lys Asp His Gln Ser Arg Asn Leu Lys Tyr Ala Ser Trp Lys Glu
 80 85 90
 Phe Ser Asp Phe Met Lys Trp Ser Ile Pro Ala Phe Leu Tyr Phe
 95 100 105
 Leu Asp Asn Leu Ile Val Phe Tyr Val Leu Ser Tyr Leu Gln Pro
 110 115 120

Ala Met Ala Val	Ile Phe Ser Asn Phe Ser	Ile Ile Thr Thr	Ala
	125	130	135
Leu Leu Phe Arg	Ile Val Leu Lys Arg Arg	Leu Asn Trp Ile	Gln
	140	145	150
Trp Ala Ser Leu	Leu Thr Leu Phe Leu Ser	Ile Val Ala Leu	Thr
	155	160	165
Ala Gly Thr Lys	Thr Leu Gln His Asn Leu	Ala Gly Arg Gly	Phe
	170	175	180
His His Asp Ala	Phe Phe Ser Pro Ser Asn	Ser Cys Leu Leu	Phe
	185	190	195
Arg Ser Glu Cys	Pro Arg Lys Asp Asn Cys	Thr Ala Lys Glu	Trp
	200	205	210
Thr Phe Pro Glu	Ala Lys Trp Asn Thr Thr	Ala Arg Val Phe	Ser
	215	220	225
His Ile Arg Leu	Gly Met Gly His Val Leu	Ile Ile Val Gln	Cys
	230	235	240
Phe Ile Ser Ser	Met Ala Asn Ile Tyr Asn	Glu Lys Ile Leu	Lys
	245	250	255
Glu Gly Asn Gln	Leu Thr Glu Ser Ile Phe	Ile Gln Asn Ser	Lys
	260	265	270
Leu Tyr Phe Phe	Gly Ile Leu Phe Asn Gly	Leu Thr Leu Gly	Leu
	275	280	285
Gln Arg Ser Asn	Arg Asp Gln Ile Lys Asn	Cys Gly Phe Phe	Tyr
	290	295	300
Gly His Ser Ala	Phe Ser Val Ala Leu Ile	Phe Val Thr Ala	Phe
	305	310	315
Gln Gly Leu Ser	Val Ala Phe Ile Leu Lys	Phe Leu Asp Asn	Met
	320	325	330
Phe His Val Leu	Met Ala Gln Val Thr Thr	Val Ile Ile Thr	Thr
	335	340	345
Val Ser Val Leu	Val Phe Asp Phe Arg Pro	Ser Leu Glu Phe	Phe
	350	355	360
Leu Glu Ala Pro	Ser Val Leu Leu Ser Ile	Phe Ile Tyr Asn	Ala
	365	370	375
Ser Lys Pro Gln	Val Pro Glu Tyr Ala Pro	Arg Gln Glu Arg	Ile
	380	385	390
Arg Asp Leu Ser	Gly Asn Leu Trp Glu Arg	Ser Ser Gly Asp	Gly
	395	400	405
Glu Glu Leu Glu	Arg Leu Thr Lys Pro Lys	Ser Asp Glu Ser	Asp
	410	415	420
Glu Asp Thr Phe			

<210> 15
 <211> 755
 <212> DNA
 <213> Homo sapiens

<400> 15
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 ctatacctac tgtagcttct ccacgtatgg accctaaagg ctactgctgc 150
 tactacgggg ctagacagtt actgtctcag ctctaggatg tgcgttcttc 200
 cactagaagc tcttctgagg gaggtaatta aaaaacagtg gaatggaaaa 250
 acagtgcgtg agtcatcctg taatatgctc cttgtcaaca atgtatacat 300
 tcctgctagg tgccatattc attgctttta gctcaagtcg catcttacta 350
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 tgtgaatgtg tgctcagaac tgggtgaagct agttttctgt gtgcttgtgt 450
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 tcctggaagg aattctctga tttcatgaag tggtcattc ctgcctttct 550
 ttatttcctg gataacttga ttgtcttcta tgtcctgtcc tatcttcaac 600
 cagccatggc tggtatcttc tcaaatttta gcattataac aacagctctt 650
 ctattcagga tagtgctgaa gaggcgtcta aactggatcc agtgggcttc 700
 cctcctgact ttatttttgt ctattgtggc cttgactgcc gggactaaaa 750
 cttta 755

<210> 16
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 16
 ctatacctac tgtagcttct 20

<210> 17
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 17
 tcagagaatt ccttccagga 20

<210> 18
 <211> 40
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 18

acagtgcctg agtcatcctg taatatgctc cttgtcaaca 40

<210> 19

<211> 2142

<212> DNA

<213> Homo sapiens

<400> 19

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cgcgcgggcg ccgtggctaa ggctgctacg aagcgagctt gggaggagca 100
gcggcctgcg gggcagagga gcatcccgtc taccaggctc caagcggcgt 150
ggcccgcggg tcatggccaa aggagaaggc gccgagagcg gctccgcggc 200
ggggctgcta cccaccagca tcctccaaag cactgaacgc ccggcccagg 250
tgaagaaaga accgaaaaag aagaaacaac agttgtctgt ttgcaacaag 300
ctttgctatg cacttggggg agccccctac cagggtgacg gctgtgccct 350
gggtttcttc cttcagatct acctattgga tgtggctcag gtgggccctt 400
tctctgcctc catcatcctg tttgtgggcc gagcctggga tgccatcaca 450
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tcgccttatg ccctggatca tcttctccac gccctggcc gtcattgcct 550
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gattctgcca cgcctatcg gatgactgtg gaagtgtggt gcacagtgtc 750
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gcgtgcggga gcagagagaa ccctatgaag ccagcagtc tgagccaatc 1000
gcctacttcc ggggcctaog gctgggtcatg agccacggcc catacatcaa 1050
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aacctcatca ttacatatgc ggtagctgtg gcagctggca tcagtgtggc 1350
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ggagaggcgg cggcagaata agaaggccct gcaggcactg agggacgagg 1700
ccagcagctc tggctgtctc gaaacagact ccacagagct ggctagcatc 1750
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gggatcagga cctgtctgcc ggcttgctga gcagctggac tgcagggtgct 1850
aggaagggaa ctgaagactc aaggaggtgg cccaggacac ttgctgtgct 1900
cactgtgggg ccggtgtctc tgtggcctcc tgcctcccct ctgcctgcct 1950
gtggggccaa gccctggggc tgccactgtg aatatgccaa ggactgatcg 2000
ggcctagccc ggaacactaa tgtagaaacc ttttttttac agagccta 2050
taataactta atgactgtgt acatagcaat gtgtgtgtat gtatatgtct 2100
gtgagctatt aatgttatta attttcataa aagctggaaa gc 2142

<210> 20
<211> 458
<212> PRT
<213> Homo sapiens

<400> 20
Met Trp Leu Arg Trp Ala Leu Ser Leu Pro Pro Ser Ser Cys Leu
1 5 10 15
Trp Ala Glu Pro Gly Met Pro Ser Gln Thr Pro Trp Trp Ala Ser
20 25 30
Ala Ser Ala Asn Pro Pro Gly Pro Ala Trp Val Ala Leu Cys Pro
35 40 45
Gly Ser Ser Ser Pro Arg Pro Trp Pro Ser Leu Pro Thr Ser Ser
50 55 60
Ser Gly Ser Cys Pro Thr Ser His Thr Ala Arg Pro Ile Gly Thr
65 70 75
Cys Phe Ser Ile Ala Ser Leu Lys Gln Trp Ser Arg Val Ser Met
80 85 90
Phe Pro Thr Arg Leu Ser Pro Cys Ser Ser Ala Thr Glu Gln Thr
95 100 105

Pro Ile Asp Glu Glu Arg Arg Arg Gln Asn Lys Lys Ala Leu Gln
 425 430 435
 Ala Leu Arg Asp Glu Ala Ser Ser Ser Gly Cys Ser Glu Thr Asp
 440 445 450
 Ser Thr Glu Leu Ala Ser Ile Leu
 455

<210> 21
 <211> 571
 <212> DNA
 <213> Homo sapiens

<400> 21
 gggaaacgca aaaggcatac ctgctggcag cggggggtcat tgtctgtatc 50
 tatataatct gtgctgtcat cctgatcctg ggcgtgcggg agcagagaga 100
 accctatgaa gccacgacgt ctgagccaat cgcctacttc cgggggcctac 150
 ggctgggtcat gagccacggc ccatacatca aacttattac tggcttcctc 200
 ttcacctcct tggctttcat gctggtggag gggaactttg tcttgttttg 250
 cacctacacc ttgggcttcc gcaatgaatt ccagaatcta ctcctggcca 300
 tcatgctctc ggccacttta accattccca tctggcagtg gttcttgacc 350
 cggtttgga agaagacagc tgtatatgtt gggatctcat cagcagtgcc 400
 atttctcatc ttggtggccc tcatggagag taacctcatc attacatatg 450
 cggtagctgt ggcagctggc atcagtggtg cagctgcctt cttactaccc 500
 tggtcgatgc tgctgatgt cattgacgac ttccatctga agcagcccca 550
 cttccatgga accgagccca t 571

<210> 22
 <211> 1173
 <212> DNA
 <213> Homo sapiens

<400> 22
 ggggcttcgg cgccagcggc cagcgctagt cggctctgga aggatttaca 50
 aaaggtgcag gtatgagcag gtctgaagac taacattttg tgaagttgta 100
 aaacagaaaa cctgttagaa atgtggtggt ttcagcaagg cctcagtttc 150
 cttccttcag cccttgtaat ttggacatct gctgctttca tattttcata 200
 cattactgca gtaacactcc accatataga cccggcttta cttatatca 250
 gtgacactgg tacagtagct ccagaaaaat gcttatttgg ggcaatgcta 300
 aatattgcgg cagttttatg cattgctacc atttatgttc gttataagca 350
 agttcatgct ctgagtcctg aagagaacgt tatcatcaaa ttaaacaagg 400
 ctggccttgt acttgaata ctgagttgtt taggactttc tattgtggca 450

aacttccaga aaacaaccct ttttgctgca catgtaagtg gagctgtgct 500
 tacctttgggt atggggtcat tatatatgtt tggtcagacc atcctttcct 550
 accaaatgca gcccaaaatc catggcaaac aagtcttctg gatcagactg 600
 ttgttggtta tctggtgtgg agtaagtgca cttagcatgc tgacttgctc 650
 atcagttttg cacagtggca attttgggac tgatttagaa cagaaactcc 700
 attggaaccc cgaggacaaa ggttatgtgc ttcacatgat cactactgca 750
 gcagaatgggt ctatgtcatt ttccttcttt gggtttttcc tgacttacat 800
 tcgtgatttt cagaaaattt ctttacgggt ggaagccaat ttacatggat 850
 taaccctcta tgacactgca ccttgcccta ttaacaatga acgaacacgg 900
 ctactttcca gagatatttg atgaaaggat aaaatatttc tgtaatgatt 950
 atgatttctca gggattgggg aaagggtcac agaagttgct tattcttctc 1000
 tgaaattttc aaccacttaa tcaaggctga cagtaacact gatgaatgct 1050
 gataatcagg aaacatgaaa gaagccattt gatagattat tctaaaggat 1100
 atcatcaaga agactattaa aaacacctat gcctatactt ttttatctca 1150
 gaaaataaag tcaaaagact atg 1173

<210> 23
 <211> 266
 <212> PRT
 <213> Homo sapiens

<400> 23
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 Val Ile Trp Thr Ser Ala Ala Phe Ile Phe Ser Tyr Ile Thr Ala
 20 25 30
 Val Thr Leu His His Ile Asp Pro Ala Leu Pro Tyr Ile Ser Asp
 35 40 45
 Thr Gly Thr Val Ala Pro Glu Lys Cys Leu Phe Gly Ala Met Leu
 50 55 60
 Asn Ile Ala Ala Val Leu Cys Ile Ala Thr Ile Tyr Val Arg Tyr
 65 70 75
 Lys Gln Val His Ala Leu Ser Pro Glu Glu Asn Val Ile Ile Lys
 80 85 90
 Leu Asn Lys Ala Gly Leu Val Leu Gly Ile Leu Ser Cys Leu Gly
 95 100 105
 Leu Ser Ile Val Ala Asn Phe Gln Lys Thr Thr Leu Phe Ala Ala
 110 115 120
 His Val Ser Gly Ala Val Leu Thr Phe Gly Met Gly Ser Leu Tyr
 125 130 135

Met	Phe	Val	Gln	Thr	Ile	Leu	Ser	Tyr	Gln	Met	Gln	Pro	Lys	Ile
				140					145					150
His	Gly	Lys	Gln	Val	Phe	Trp	Ile	Arg	Leu	Leu	Leu	Val	Ile	Trp
				155					160					165
Cys	Gly	Val	Ser	Ala	Leu	Ser	Met	Leu	Thr	Cys	Ser	Ser	Val	Leu
				170					175					180
His	Ser	Gly	Asn	Phe	Gly	Thr	Asp	Leu	Glu	Gln	Lys	Leu	His	Trp
				185					190					195
Asn	Pro	Glu	Asp	Lys	Gly	Tyr	Val	Leu	His	Met	Ile	Thr	Thr	Ala
				200					205					210
Ala	Glu	Trp	Ser	Met	Ser	Phe	Ser	Phe	Phe	Gly	Phe	Phe	Leu	Thr
				215					220					225
Tyr	Ile	Arg	Asp	Phe	Gln	Lys	Ile	Ser	Leu	Arg	Val	Glu	Ala	Asn
				230					235					240
Leu	His	Gly	Leu	Thr	Leu	Tyr	Asp	Thr	Ala	Pro	Cys	Pro	Ile	Asn
				245					250					255
Asn	Glu	Arg	Thr	Arg	Leu	Leu	Ser	Arg	Asp	Ile				
				260					265					

<210> 24
 <211> 485
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 14, 484
 <223> unknown base

<400> 24
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 ctgatgcoga gttccgtctc tcgggtcttt tcttgggtccc aggcmaaagcg 100
 gagcggagat cctcaaacgg cctagtgcct cgcgcttccg gagaaaatca 150
 gcgggtctaataattcctct ggtttgttga agcagttacc aagaatcttc 200
 aaccctttcc cacaaaagct aattgagtac acgttctctg tgagtacacg 250
 ttctgtttga ttacaaaag gtgcaggtat gagcaggtct gaagactaac 300
 attttgtgaa gttgtaaaac agaaaacctg ttagaaatgt ggtgggtttca 350
 gcaaggcctc agtttccttc cttcagccct tgtaatttgg acatctgctg 400
 ctttcatatt ttcatacatt actgcagtaa cactccacca tatagacccg 450
 gctttacctt atatcagtga cactggtaca gtanc 485

<210> 25
 <211> 40
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe
 <400> 25
 acctgtaga aatgtggtg tttcagcaag gcctcagttt 40

<210> 26
 <211> 46
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 26
 ggagatagct gctatgggtt cttcaggcac aacttaacat gggaag 46

<210> 27
 <211> 1399
 <212> DNA
 <213> Homo sapiens

<400> 27
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 ctgccccgcg ggccgggggtg cggagccgac atgcgccccgc ttctcggcct 100
 ccttctggtc ttccgcccgt gcaccttcgc cttgtacttg ctgtcgacgc 150
 gactgccccg cgggcccggaga ctgggctcca ccgaggaggc tggaggcagg 200
 tcgctgtggt tcccctccga cctggcagag ctgcgggagc tctctgaggt 250
 ccttcgagag taccggaagg agcaccaggc ctacgtgttc ctgctcttct 300
 gcggcgcccta cctctacaaa cagggtttg ccatccccgc ctccagcttc 350
 ctgaatgttt tagctgggtgc cttgtttggg ccatggctgg ggcttctgct 400
 gtgctgtgtg ttgacctcgg tgggtgccac atgctgtctac ctgctctcca 450
 gtatttttgg caaacagttg gtggtgtcct actttcctga taaagtggcc 500
 ctgctgcaga gaaaggtgga ggagaacaga aacagcttgt tttttttctt 550
 attgtttttg agacttttcc ccatgacacc aaactgggtc ttgaacctct 600
 cggccccaat tctgaacatt cccatcgtgc agttcttctt ctcaattctt 650
 atcggtttga tcccatataa tttcatctgt gtgcagacag ggtccatcct 700
 gtcaacccta acctctctgg atgctctttt ctctggggac actgtcttta 750
 agctgttggc cattgccatg gtggcattaa ttcctggaac cctcattaaa 800
 aaatttagtc agaaacatct gcaattgaat gaaacaagta ctgctaata 850
 tatacacagt agaaaagaca catgatctgg attttctgtt tgccacatcc 900
 ctggactcag ttgcttattt gtgtaatgga tgtggtcctc taaagcccct 950
 cattgttttt gattgccttc tataggtgat gtggacactg tgcataaatg 1000

tgcagtgtct tttcagaaag gacactctgc tcttgaaggt gtattacatc 1050
 aggttttcaa accagccctg gtgtagcaga cactgcaaca gatgcctcct 1100
 agaaaatgct gtttgtggcc gggcgcggtg gctcacgcct gtaatcccag 1150
 cactttggga ggccgaggcc ggtgattcac aaggtcagga gttcaagacc 1200
 agcctggcca agatggtgaa atcctgtctc taataaaaat acaaaaatta 1250
 gccaggcgtg gtggcaggca cctgtaatcc cagctactcg ggaggctgag 1300
 gcaggagaat tgcttgaacc aaggtggcag aggttgcaat aagccaagat 1350
 cacaccactg cactccagcc tgggtgatag agtgagacac tgtcttgac 1399

<210> 28
 <211> 264
 <212> PRT
 <213> Homo sapiens

<400> 28
 Met Arg Pro Leu Leu Gly Leu Leu Leu Val Phe Ala Gly Cys Thr
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 Phe Ala Leu Tyr Leu Leu Ser Thr Arg Leu Pro Arg Gly Arg Arg
 20 25 30
 Leu Gly Ser Thr Glu Glu Ala Gly Gly Arg Ser Leu Trp Phe Pro
 35 40 45
 Ser Asp Leu Ala Glu Leu Arg Glu Leu Ser Glu Val Leu Arg Glu
 50 55 60
 Tyr Arg Lys Glu His Gln Ala Tyr Val Phe Leu Leu Phe Cys Gly
 65 70 75
 Ala Tyr Leu Tyr Lys Gln Gly Phe Ala Ile Pro Gly Ser Ser Phe
 80 85 90
 Leu Asn Val Leu Ala Gly Ala Leu Phe Gly Pro Trp Leu Gly Leu
 95 100 105
 Leu Leu Cys Cys Val Leu Thr Ser Val Gly Ala Thr Cys Cys Tyr
 110 115 120
 Leu Leu Ser Ser Ile Phe Gly Lys Gln Leu Val Val Ser Tyr Phe
 125 130 135
 Pro Asp Lys Val Ala Leu Leu Gln Arg Lys Val Glu Glu Asn Arg
 140 145 150
 Asn Ser Leu Phe Phe Phe Leu Leu Phe Leu Arg Leu Phe Pro Met
 155 160 165
 Thr Pro Asn Trp Phe Leu Asn Leu Ser Ala Pro Ile Leu Asn Ile
 170 175 180
 Pro Ile Val Gln Phe Phe Phe Ser Val Leu Ile Gly Leu Ile Pro
 185 190 195
 Tyr Asn Phe Ile Cys Val Gln Thr Gly Ser Ile Leu Ser Thr Leu
 200 205 210

Thr	Ser	Leu	Asp	Ala	Leu	Phe	Ser	Trp	Asp	Thr	Val	Phe	Lys	Leu
				215					220					225
Leu	Ala	Ile	Ala	Met	Val	Ala	Leu	Ile	Pro	Gly	Thr	Leu	Ile	Lys
				230					235					240
Lys	Phe	Ser	Gln	Lys	His	Leu	Gln	Leu	Asn	Glu	Thr	Ser	Thr	Ala
				245					250					255
Asn	His	Ile	His	Ser	Arg	Lys	Asp	Thr						
				260										

<210> 29
 <211> 1292
 <212> DNA
 <213> Homo sapiens

<400> 29
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 gtcaatcatt ttccagttct cagccgctca gttgtgatca agggacacgt 100
 gggtttccgaa ctgccagctc agaataggaa aataacttgg gattttatat 150
 tggaagacat ggatcttgct gccaacgaga tcagcattta tgacaaactt 200
 tcagagactg ttgatttggg gagacagacc ggccatcagt gtggcatgtc 250
 agagaaggca attgaaaaat ttatcagaca gctgctggaa aagaatgaac 300
 ctccagagacc cccccgcgag tatcctctcc ttatagttgt gtataagggt 350
 ctcgcaacct tgggattaat cttgctcact gcctactttg tgattcaacc 400
 tttcagccca ttagcacctg agccagtgtt ttctggagct cacacctggc 450
 gctcactcat ccatcacatt aggctgatgt ccttgcccat tgccaagaag 500
 tacatgtcag aaaataaggg agttcctctg catgggggtg atgaagacag 550
 accctttcca gactttgacc cctggtggac aaacgactgt gagcagaatg 600
 agtcagagcc cattcctgcc aactgcaactg gctgtgcca gaaacacctg 650
 aagggtgatgc tccctggaaga cggcccaagg aaatttgaga ggctccatcc 700
 actggtgatc aagacgggaa agccctgtt ggaggaagag attcagcatt 750
 ttttgtgcca gtaccctgag ggcacagaag gcttctctga agggtttttc 800
 gccaaagtggg ggcgctgctt tccctgagcg tggttcccat ttccttatcc 850
 atggaggaga cctctgaaca gatcacaat gttacgtgag ctttttctctg 900
 ttttcaactca cctgccattt ccaaaagatg cctctttaa caagtgtctc 950
 tttcttcacc cagaacctgt tgtggggagt aagatgcata agatgcctga 1000
 cctatttata attggcagcg gtgaggccat gttgcagctc atcctccct 1050
 tccagtgccg aagacattgt cagtctgtgg ccatgccaat agagccaggg 1100
 gatatcggt atgtcgacac caccactgg aaggtctacg ttatagccag 1150

aggggtccag cctttgggtca tctgcatgg aaccgctttc tcagaactgt 1200
 aggaaataga actgtgcaca ggaacagctt ccagagccga aaaccaggtt 1250
 gaaaggggaa aaataaaaac aaaaacgatg aaactgcaaa aa 1292

<210> 30
 <211> 347
 <212> PRT
 <213> Homo sapiens

<400> 30
 Met Asp Leu Ala Ala Asn Glu Ile Ser Ile Tyr Asp Lys Leu Ser
 1 5 10 15
 Glu Thr Val Asp Leu Val Arg Gln Thr Gly His Gln Cys Gly Met
 20 25 30
 Ser Glu Lys Ala Ile Glu Lys Phe Ile Arg Gln Leu Leu Glu Lys
 35 40 45
 Asn Glu Pro Gln Arg Pro Pro Pro Gln Tyr Pro Leu Leu Ile Val
 50 55 60
 Val Tyr Lys Val Leu Ala Thr Leu Gly Leu Ile Leu Leu Thr Ala
 65 70 75
 Tyr Phe Val Ile Gln Pro Phe Ser Pro Leu Ala Pro Glu Pro Val
 80 85 90
 Leu Ser Gly Ala His Thr Trp Arg Ser Leu Ile His His Ile Arg
 95 100 105
 Leu Met Ser Leu Pro Ile Ala Lys Lys Tyr Met Ser Glu Asn Lys
 110 115 120
 Gly Val Pro Leu His Gly Gly Asp Glu Asp Arg Pro Phe Pro Asp
 125 130 135
 Phe Asp Pro Trp Trp Thr Asn Asp Cys Glu Gln Asn Glu Ser Glu
 140 145 150
 Pro Ile Pro Ala Asn Cys Thr Gly Cys Ala Gln Lys His Leu Lys
 155 160 165
 Val Met Leu Leu Glu Asp Ala Pro Arg Lys Phe Glu Arg Leu His
 170 175 180
 Pro Leu Val Ile Lys Thr Gly Lys Pro Leu Leu Glu Glu Glu Ile
 185 190 195
 Gln His Phe Leu Cys Gln Tyr Pro Glu Ala Thr Glu Gly Phe Ser
 200 205 210
 Glu Gly Phe Phe Ala Lys Trp Trp Arg Cys Phe Pro Glu Arg Trp
 215 220 225
 Phe Pro Phe Pro Tyr Pro Trp Arg Arg Pro Leu Asn Arg Ser Gln
 230 235 240
 Met Leu Arg Glu Leu Phe Pro Val Phe Thr His Leu Pro Phe Pro
 245 250 255

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Lys	Asp	Ala	Ser	Leu	Asn	Lys	Cys	Ser	Phe	Leu	His	Pro	Glu	Pro
				260					265					270
Val	Val	Gly	Ser	Lys	Met	His	Lys	Met	Pro	Asp	Leu	Phe	Ile	Ile
				275					280					285
Gly	Ser	Gly	Glu	Ala	Met	Leu	Gln	Leu	Ile	Pro	Pro	Phe	Gln	Cys
				290					295					300
Arg	Arg	His	Cys	Gln	Ser	Val	Ala	Met	Pro	Ile	Glu	Pro	Gly	Asp
				305					310					315
Ile	Gly	Tyr	Val	Asp	Thr	Thr	His	Trp	Lys	Val	Tyr	Val	Ile	Ala
				320					325					330
Arg	Gly	Val	Gln	Pro	Leu	Val	Ile	Cys	Asp	Gly	Thr	Ala	Phe	Ser
				335					340					345

Glu Leu

<210> 31
 <211> 478
 <212> DNA
 <213> Homo sapiens

<400> 31
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 gcccgagggg cgcgagcccc gcatgaatca ttgtagtcaa tcattttcca 100
 gttctcagcc gttcagttgt gatcaaggga cacgtggttt ccgaactgcc 150
 agctcagaat aggaaaataa cttgggattt tatattggaa gacatggatc 200
 ttgctgccaa cgagatcagc atttatgaca aactttcaga gactgttgat 250
 ttggtgagac agaccggcca tcagtgtggc atgtcagaga aggcaattga 300
 aaaatttatc agacagctgc tggaaaagaa tgaacctcag agaccccccc 350
 cgcagtatcc tctccttata gttgtgtata aggttctcgc aaccttggga 400
 ttaatcttgc tcaactgccta ctttgtgatt caacctttca gccatttagc 450
 acctgagcca gtgctttgtg gagctcac 478

<210> 32
 <211> 3531
 <212> DNA
 <213> Homo sapiens

<400> 32
 cccacgcgtc cgcccacgcg tccggctgaa cacctcttct ttggagtcag 50
 ccaactgatga ggcaggggtcc ccaacttcag ctgcagcagc tgcagcagct 100
 gcagagcgct gtcctgggt ggtgccactg gtgcgcacgc tgctagaccg 150
 tgcctatgag ccgctggggc tgcagtgggg actgccctcc ctgccacca 200
 ccaatggcag cccaccttc tttgaagact tccaggttt ttgtgccaca 250

cccgaatggc gccacttcat cgacaaacag gtacagccaa ccatgtccca 300
 gttcgaaatg gacacgtatg ctaagagcca cgaccttatg tcagggtttct 350
 ggaatgcctg ctatgacatg cttatgagca gtgggcagcg gcgccagtgg 400
 gagcgcgccc agagtcgtcg ggccttccag gagctggtgc tggaacctgc 450
 gcagaggcgg gcgcgcctgg aggggctacg ctacacggca gtgctgaagc 500
 agcaggcaac gcagcactcc atggccctgc tgcactgggg ggcgctgtgg 550
 cgccagctcg ccagcccatg tggggcctgg gcgctgaggg aactcccat 600
 cccccgctgg aaactgtcca gcgccgagac atattcacgc atgcgtctga 650
 agctggtgcc caaccatcac ttcgaccctc acctggaagc cagcgctctc 700
 cgagacaatc tgggtgaggt tcccctgaca cccaccgagg aggcctcact 750
 gcctctggca gtgaccaaag aggccaaagt gagcaccca cccgagttgc 800
 tgcaggagga ccagctcggc gaggacgagc tggctgagct ggagaccccg 850
 atggaggcag cagaactgga tgagcagcgt gagaagctgg tgctgtcggc 900
 cgagtgccag ctggtgacgg tagtggccgt ggtcccaggg ctgctggagg 950
 tcaccacaca gaatgtatac ttctacgatg gcagcactga gcgcgtggaa 1000
 accgaggagg gcacgggcta tgatttcggc cgcccactgg ccagctgcg 1050
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 tctttatoga tcaggccaac tacttctca acttcccatg caagggtgggc 1150
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 catccccccc catacccagg tacggaacca ggtgtactcg tggctcctgc 1250
 gcctacggcc cccctctcaa ggctacctaa gcagccgctc ccccaggag 1300
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 atgacctgtc tcagtacct gtgttccctt gggctcctgca ggactacgtg 1450
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 acccactact ccaatgcagc aggcgtgatg cactacctca tccgcgtgga 1650
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 agccctgccg atgtgaagga gctcatccc gaattcttct actttcctga 1800
 cttcctggag aaccagaacg gttttgacct gggctgtctc cagctgacca 1850

acgagaaggt aggcgatgtg gtgctacccc cgtgggcccag ctctcctgag 1900
 gacttcatcc agcagcaccg ccaggctctg gagtcggagt atgtgtctgc 1950
 acacctacac gagtggatcg acctcatctt tggctacaag cagcgggggc 2000
 cagccgccga ggaggccctc aatgtcttct attactgcac ctatgagggg 2050
 gctgtagacc tggaccatgt gacagatgag cgggaacgga aggctctgga 2100
 gggcattatc agcaactttg ggcagactcc ctgtcagctg ctgaaggagc 2150
 cacatccaac tcggctctca gctgaggaag cagcccatcg ccttgcacgc 2200
 ctggacacta actcacctag catcttccag cacctggacg aactcaaggc 2250
 attcttcgca gaggtgactg tgagtgccag tgggctgctg ggcacccaca 2300
 gctggttgcc ctatgaccgc aacataagca actacttcag cttcagcaaa 2350
 gaccccacca tgggcagcca caagacgcag cgactgctga gtggcccgtg 2400
 ggtgccaggc agtgggtgtga gtggacaagc actggcagtg gccccggatg 2450
 gaaagctgct attcagcggg gccactggg atggcagcct gcgggtgact 2500
 gcactacccc gtggcaagct gttgagccag ctgagctgcc accttgatgt 2550
 agtaacctgc cttgcactgg acacctgtgg catctacctc atctcaggct 2600
 cccgggacac cacgtgcatg gtgtggcggc tcctgcatca ggggtggtctg 2650
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 tgcagtgagc tgtgtggcca tcagcactga acttgacatg gctgtgtctg 2750
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 gtagcggcac tacggcctct gggtgccaca ttccctggac ctattttcca 2850
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 aacgtcctgg ggcccaggtc acctactcct tgcacctgta ttcagtcaat 2950
 gggaagttgc gggcttcact gccctggca gagcagccta cagccctgac 3000
 ggtgacagag gactttgtgt tgctgggcac cgcccagtgc gccctgcaca 3050
 tcctccaact aaacacactg ctcccggccg cgcctccctt gcccatgaag 3100
 gtggccatcc gcagcgtggc cgtgaccaag gagcgcagcc acgtgctggt 3150
 gggcctggag gatggcaagc tcatcgtggt ggtcgcgggg cagccctctg 3200
 aggtgcgcag cagccagttc gcgcggaagc tgtggcggtc ctgcgcgcgc 3250
 atctcccagg tgtcctcggg agagacggaa tacaacccta ctgaggcgcg 3300
 ctgaacctgg ccagtccggc tgctcgggcc ccgccccggg caggcctggc 3350
 ccgggaggcc ccgcccagaa gtcggcggga acaccccggg gtgggcagcc 3400
 cagggggtga gcggggccca ccctgccag ctcagggtt ggcgggcgat 3450

gttaccacct cagggattgg cgggcggaag tcccggccct cgccggctga 3500
 ggggccgccc tgaggccag cactggcgtc t 3531

<210> 33
 <211> 1003
 <212> PRT
 <213> Homo sapiens

<400> 33
 Met Ser Gln Phe Glu Met Asp Thr Tyr Ala Lys Ser His Asp Leu
 1 5 10 15
 Met Ser Gly Phe Trp Asn Ala Cys Tyr Asp Met Leu Met Ser Ser
 20 25 30
 Gly Gln Arg Arg Gln Trp Glu Arg Ala Gln Ser Arg Arg Ala Phe
 35 40 45
 Gln Glu Leu Val Leu Glu Pro Ala Gln Arg Arg Ala Arg Leu Glu
 50 55 60
 Gly Leu Arg Tyr Thr Ala Val Leu Lys Gln Gln Ala Thr Gln His
 65 70 75
 Ser Met Ala Leu Leu His Trp Gly Ala Leu Trp Arg Gln Leu Ala
 80 85 90
 Ser Pro Cys Gly Ala Trp Ala Leu Arg Asp Thr Pro Ile Pro Arg
 95 100 105
 Trp Lys Leu Ser Ser Ala Glu Thr Tyr Ser Arg Met Arg Leu Lys
 110 115 120
 Leu Val Pro Asn His His Phe Asp Pro His Leu Glu Ala Ser Ala
 125 130 135
 Leu Arg Asp Asn Leu Gly Glu Val Pro Leu Thr Pro Thr Glu Glu
 140 145 150
 Ala Ser Leu Pro Leu Ala Val Thr Lys Glu Ala Lys Val Ser Thr
 155 160 165
 Pro Pro Glu Leu Leu Gln Glu Asp Gln Leu Gly Glu Asp Glu Leu
 170 175 180
 Ala Glu Leu Glu Thr Pro Met Glu Ala Ala Glu Leu Asp Glu Gln
 185 190 195
 Arg Glu Lys Leu Val Leu Ser Ala Glu Cys Gln Leu Val Thr Val
 200 205 210
 Val Ala Val Val Pro Gly Leu Leu Glu Val Thr Thr Gln Asn Val
 215 220 225
 Tyr Phe Tyr Asp Gly Ser Thr Glu Arg Val Glu Thr Glu Glu Gly
 230 235 240
 Ile Gly Tyr Asp Phe Arg Arg Pro Leu Ala Gln Leu Arg Glu Val
 245 250 255
 His Leu Arg Arg Phe Asn Leu Arg Arg Ser Ala Leu Glu Leu Phe
 260 265 270

CCGCGGCTGA 3500

Phe	Ile	Asp	Gln	Ala	Asn	Tyr	Phe	Leu	Asn	Phe	Pro	Cys	Lys	Val	
				275					280					285	
Gly	Thr	Thr	Pro	Val	Ser	Ser	Pro	Ser	Gln	Thr	Pro	Arg	Pro	Gln	
				290					295					300	
Pro	Gly	Pro	Ile	Pro	Pro	His	Thr	Gln	Val	Arg	Asn	Gln	Val	Tyr	
				305					310					315	
Ser	Trp	Leu	Leu	Arg	Leu	Arg	Pro	Pro	Ser	Gln	Gly	Tyr	Leu	Ser	
				320					325					330	
Ser	Arg	Ser	Pro	Gln	Glu	Met	Leu	Arg	Ala	Ser	Gly	Leu	Thr	Gln	
				335					340					345	
Lys	Trp	Val	Gln	Arg	Glu	Ile	Ser	Asn	Phe	Glu	Tyr	Leu	Met	Gln	
				350					355					360	
Leu	Asn	Thr	Ile	Ala	Gly	Arg	Thr	Tyr	Asn	Asp	Leu	Ser	Gln	Tyr	
				365					370					375	
Pro	Val	Phe	Pro	Trp	Val	Leu	Gln	Asp	Tyr	Val	Ser	Pro	Thr	Leu	
				380					385					390	
Asp	Leu	Ser	Asn	Pro	Ala	Val	Phe	Arg	Asp	Leu	Ser	Lys	Pro	Ile	
				395					400					405	
Gly	Val	Val	Asn	Pro	Lys	His	Ala	Gln	Leu	Val	Arg	Glu	Lys	Tyr	
				410					415					420	
Glu	Ser	Phe	Glu	Asp	Pro	Ala	Gly	Thr	Ile	Asp	Lys	Phe	His	Tyr	
				425					430					435	
Gly	Thr	His	Tyr	Ser	Asn	Ala	Ala	Gly	Val	Met	His	Tyr	Leu	Ile	
				440					445					450	
Arg	Val	Glu	Pro	Phe	Thr	Ser	Leu	His	Val	Gln	Leu	Gln	Ser	Gly	
				455					460					465	
Arg	Phe	Asp	Cys	Ser	Asp	Arg	Gln	Phe	His	Ser	Val	Ala	Ala	Ala	
				470					475					480	
Trp	Gln	Ala	Arg	Leu	Glu	Ser	Pro	Ala	Asp	Val	Lys	Glu	Leu	Ile	
				485					490					495	
Pro	Glu	Phe	Phe	Tyr	Phe	Pro	Asp	Phe	Leu	Glu	Asn	Gln	Asn	Gly	
				500					505					510	
Phe	Asp	Leu	Gly	Cys	Leu	Gln	Leu	Thr	Asn	Glu	Lys	Val	Gly	Asp	
				515					520					525	
Val	Val	Leu	Pro	Pro	Trp	Ala	Ser	Ser	Pro	Glu	Asp	Phe	Ile	Gln	
				530					535					540	
Gln	His	Arg	Gln	Ala	Leu	Glu	Ser	Glu	Tyr	Val	Ser	Ala	His	Leu	
				545					550					555	
His	Glu	Trp	Ile	Asp	Leu	Ile	Phe	Gly	Tyr	Lys	Gln	Arg	Gly	Pro	
				560					565					570	
Ala	Ala	Glu	Glu	Ala	Leu	Asn	Val	Phe	Tyr	Tyr	Cys	Thr	Tyr	Glu	
				575					580					585	

Gly	Ala	Val	Asp	Leu	Asp	His	Val	Thr	Asp	Glu	Arg	Glu	Arg	Lys	
				590					595					600	
Ala	Leu	Glu	Gly	Ile	Ile	Ser	Asn	Phe	Gly	Gln	Thr	Pro	Cys	Gln	
				605					610					615	
Leu	Leu	Lys	Glu	Pro	His	Pro	Thr	Arg	Leu	Ser	Ala	Glu	Glu	Ala	
				620					625					630	
Ala	His	Arg	Leu	Ala	Arg	Leu	Asp	Thr	Asn	Ser	Pro	Ser	Ile	Phe	
				635					640					645	
Gln	His	Leu	Asp	Glu	Leu	Lys	Ala	Phe	Phe	Ala	Glu	Val	Thr	Val	
				650					655					660	
Ser	Ala	Ser	Gly	Leu	Leu	Gly	Thr	His	Ser	Trp	Leu	Pro	Tyr	Asp	
				665					670					675	
Arg	Asn	Ile	Ser	Asn	Tyr	Phe	Ser	Phe	Ser	Lys	Asp	Pro	Thr	Met	
				680					685					690	
Gly	Ser	His	Lys	Thr	Gln	Arg	Leu	Leu	Ser	Gly	Pro	Trp	Val	Pro	
				695					700					705	
Gly	Ser	Gly	Val	Ser	Gly	Gln	Ala	Leu	Ala	Val	Ala	Pro	Asp	Gly	
				710					715					720	
Lys	Leu	Leu	Phe	Ser	Gly	Gly	His	Trp	Asp	Gly	Ser	Leu	Arg	Val	
				725					730					735	
Thr	Ala	Leu	Pro	Arg	Gly	Lys	Leu	Leu	Ser	Gln	Leu	Ser	Cys	His	
				740					745					750	
Leu	Asp	Val	Val	Thr	Cys	Leu	Ala	Leu	Asp	Thr	Cys	Gly	Ile	Tyr	
				755					760					765	
Leu	Ile	Ser	Gly	Ser	Arg	Asp	Thr	Thr	Cys	Met	Val	Trp	Arg	Leu	
				770					775					780	
Leu	His	Gln	Gly	Gly	Leu	Ser	Val	Gly	Leu	Ala	Pro	Lys	Pro	Val	
				785					790					795	
Gln	Val	Leu	Tyr	Gly	His	Gly	Ala	Ala	Val	Ser	Cys	Val	Ala	Ile	
				800					805					810	
Ser	Thr	Glu	Leu	Asp	Met	Ala	Val	Ser	Gly	Ser	Glu	Asp	Gly	Thr	
				815					820					825	
Val	Ile	Ile	His	Thr	Val	Arg	Arg	Gly	Gln	Phe	Val	Ala	Ala	Leu	
				830					835					840	
Arg	Pro	Leu	Gly	Ala	Thr	Phe	Pro	Gly	Pro	Ile	Phe	His	Leu	Ala	
				845					850					855	
Leu	Gly	Ser	Glu	Gly	Gln	Ile	Val	Val	Gln	Ser	Ser	Ala	Trp	Glu	
				860					865					870	
Arg	Pro	Gly	Ala	Gln	Val	Thr	Tyr	Ser	Leu	His	Leu	Tyr	Ser	Val	
				875					880					885	
Asn	Gly	Lys	Leu	Arg	Ala	Ser	Leu	Pro	Leu	Ala	Glu	Gln	Pro	Thr	
				890					895					900	

Ala	Leu	Thr	Val	Thr	Glu	Asp	Phe	Val	Leu	Leu	Gly	Thr	Ala	Gln
				905					910					915
Cys	Ala	Leu	His	Ile	Leu	Gln	Leu	Asn	Thr	Leu	Leu	Pro	Ala	Ala
				920					925					930
Pro	Pro	Leu	Pro	Met	Lys	Val	Ala	Ile	Arg	Ser	Val	Ala	Val	Thr
				935					940					945
Lys	Glu	Arg	Ser	His	Val	Leu	Val	Gly	Leu	Glu	Asp	Gly	Lys	Leu
				950					955					960
Ile	Val	Val	Val	Ala	Gly	Gln	Pro	Ser	Glu	Val	Arg	Ser	Ser	Gln
				965					970					975
Phe	Ala	Arg	Lys	Leu	Trp	Arg	Ser	Ser	Arg	Arg	Ile	Ser	Gln	Val
				980					985					990
Ser	Ser	Gly	Glu	Thr	Glu	Tyr	Asn	Pro	Thr	Glu	Ala	Arg		
				995					1000					

<210> 34
 <211> 43
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 34
 tgactgcact acccctgtggc aagctgttga gccagctcag ctg 43

<210> 35
 <211> 1395
 <212> DNA
 <213> Homo sapiens

<400> 35
 cggacgcgtg ggcggacgcg tgggggctgt gagaaagtgc caataaatac 50
 atcatgcaac cccacggccc accttgtgaa ctctctgtgc ccagggtga 100
 tgtgctctt ccagggtac tcatcaaag gcctaatacca acgttctgtc 150
 ttcaatctgc aaatctatg ggtcctggg ctcttctgga cccttaactg 200
 ggtactggcc ctgggccaat gcgtcctgc tggagccttt gcctccttct 250
 actgggcctt ccacaagccc caggacatcc ctacctccc cttaatctct 300
 gccttcatcc gcacactccg ttaccacact ggtcatttg catttgagc 350
 cctcatctg acccttgtgc agatagccc ggtcatcttg gagtatattg 400
 accacaagct cagaggagtg cagaaccctg tagcccgctg catcatgtgc 450
 tgtttcaagt gctgcctctg gtgtctggaa aaatttatca agttcctaaa 500
 ccgcaatgca tacatcatga tcgccatcta cgggaagaat ttctgtgtct 550
 cagccaaaaa tgcgttcatg ctactcatgc gaaacattgt cagggtgggc 600
 gtctggaca aagtcacaga cctgtgtctg ttctttggga agctgtggt 650

Lys	Leu	Arg	Gly	Val	Gln	Asn	Pro	Val	Ala	Arg	Cys	Ile	Met	Cys	
				140					145					150	
Cys	Phe	Lys	Cys	Cys	Leu	Trp	Cys	Leu	Glu	Lys	Phe	Ile	Lys	Phe	
				155					160					165	
Leu	Asn	Arg	Asn	Ala	Tyr	Ile	Met	Ile	Ala	Ile	Tyr	Gly	Lys	Asn	
				170					175					180	
Phe	Cys	Val	Ser	Ala	Lys	Asn	Ala	Phe	Met	Leu	Leu	Met	Arg	Asn	
				185					190					195	
Ile	Val	Arg	Val	Val	Val	Leu	Asp	Lys	Val	Thr	Asp	Leu	Leu	Leu	
				200					205					210	
Phe	Phe	Gly	Lys	Leu	Leu	Val	Val	Gly	Gly	Val	Gly	Val	Leu	Ser	
				215					220					225	
Phe	Phe	Phe	Phe	Ser	Gly	Arg	Ile	Pro	Gly	Leu	Gly	Lys	Asp	Phe	
				230					235					240	
Lys	Ser	Pro	His	Leu	Asn	Tyr	Tyr	Trp	Leu	Pro	Ile	Met	Thr	Ser	
				245					250					255	
Ile	Leu	Gly	Ala	Tyr	Val	Ile	Ala	Ser	Gly	Phe	Phe	Ser	Val	Phe	
				260					265					270	
Gly	Met	Cys	Val	Asp	Thr	Leu	Phe	Leu	Cys	Phe	Leu	Glu	Asp	Leu	
				275					280					285	
Glu	Arg	Asn	Asn	Gly	Ser	Leu	Asp	Arg	Pro	Tyr	Tyr	Met	Ser	Lys	
				290					295					300	
Ser	Leu	Leu	Lys	Ile	Leu	Gly	Lys	Lys	Asn	Glu	Ala	Pro	Pro	Asp	
				305					310					315	
Asn	Lys	Lys	Arg	Lys	Lys										
				320											

<210> 37
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 37
 tcgtgccag gggctgatgt gc 22

<210> 38
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 38
 gtctttaccc agccccggga tgcg 24

<210> 39
 <211> 50

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 39
ggcctaatacc aacgttctgt cttcaatctg caaatctatg gggtcctggg 50

<210> 40
<211> 1365
<212> DNA
<213> Homo sapiens

<400> 40
gagtcttgac cgccgccggg ctcttggtac ctcagcgca gcgccaggcg 50
tcgggccgcc gtggctatgt tcgtgtccga tttccgcaaa gagttctacg 100
agggtggtcca gagccagagg gtcccttctc tcgtggcctc ggacgtggat 150
gctctgtgtg cgtgcaagat ccttcaggcc ttgttccagt gtgaccacgt 200
gcaatatacg ctggttccag tttctgggtg gcaagaactt gaaactgcat 250
ttcttgagca taaagaacag tttcattatt ttattctcat aaactgtgga 300
gctaattgtag acctattgga tattcttcaa cctgatgaag aactatatt 350
ctttgtgtgt gactccata ggccagtcaa tgtcgtcaat gtatacaacg 400
ataccagat caaattactc attaaacaag atgatgacct tgaagttccc 450
gcctatgaag acatcttcag ggatgaagag gaggatgaag agcattcagg 500
aaatgacagt gatgggtcag agccttctga gaagcgaca cggttagaag 550
aggagatagt ggagcaaacc atgcggagga ggcagcggcg agagtgggag 600
gcccggagaa gagacatcct ctttgactac gagcagtatg aatatcatgg 650
gacatcgtca gccatggtga tgtttgagct ggcttgatg ctgtccaagg 700
acctgaatga catgctgtgg tgggccatcg ttggactaac agaccagtgg 750
gtgcaagaca agatcactca aatgaaatac gtgactgatg ttggtgtcct 800
gcagcgccac gtttcccgcc acaaccaccg gaacgaggat gaggagaaca 850
cactctccgt ggactgcaca cggatctcct ttgagtatga cctccgcctg 900
gtgctctacc agcactggtc cctccatgac agcctgtgca acaccagcta 950
taccgcagcc aggttcaagc tgtggtctgt gcatggacag aagcggctcc 1000
aggagtccct tgcagacatg ggtcttcccc tgaagcaggt gaagcagaag 1050
ttccaggcca tggacatctc cttgaaggag aatttgcggg aaatgattga 1100
agagtctgca aataaatttg ggatgaagga catgcgcgtg cagactttca 1150
gcattcattt tgggttcaag cacaagtttc tggccagcga cgtggtcttt 1200

gccacccatgt ctttgatgga gagccccgag aaggatggct cagggacaga 1250
 tcacttcacac caggctctgg acagcctctc caggagtaac ctggacaagc 1300
 tgtaccatgg cctggaactc gccagaagc agctgcgagc caccagcag 1350
 accattgcca gctgc 1365

<210> 41
 <211> 566
 <212> PRT
 <213> Homo sapiens

<400> 41
 Met Phe Val Ser Asp Phe Arg Lys Glu Phe Tyr Glu Val Val Gln
 1 5 10 15
 Ser Gln Arg Val Leu Leu Phe Val Ala Ser Asp Val Asp Ala Leu
 20 25 30
 Cys Ala Cys Lys Ile Leu Gln Ala Leu Phe Gln Cys Asp His Val
 35 40 45
 Gln Tyr Thr Leu Val Pro Val Ser Gly Trp Gln Glu Leu Glu Thr
 50 55 60
 Ala Phe Leu Glu His Lys Glu Gln Phe His Tyr Phe Ile Leu Ile
 65 70 75
 Asn Cys Gly Ala Asn Val Asp Leu Leu Asp Ile Leu Gln Pro Asp
 80 85 90
 Glu Asp Thr Ile Phe Phe Val Cys Asp Ser His Arg Pro Val Asn
 95 100 105
 Val Val Asn Val Tyr Asn Asp Thr Gln Ile Lys Leu Leu Ile Lys
 110 115 120
 Gln Asp Asp Asp Leu Glu Val Pro Ala Tyr Glu Asp Ile Phe Arg
 125 130 135
 Asp Glu Glu Glu Asp Glu Glu His Ser Gly Asn Asp Ser Asp Gly
 140 145 150
 Ser Glu Pro Ser Glu Lys Arg Thr Arg Leu Glu Glu Glu Ile Val
 155 160 165
 Glu Gln Thr Met Arg Arg Arg Gln Arg Arg Glu Trp Glu Ala Arg
 170 175 180
 Arg Arg Asp Ile Leu Phe Asp Tyr Glu Gln Tyr Glu Tyr His Gly
 185 190 195
 Thr Ser Ser Ala Met Val Met Phe Glu Leu Ala Trp Met Leu Ser
 200 205 210
 Lys Asp Leu Asn Asp Met Leu Trp Trp Ala Ile Val Gly Leu Thr
 215 220 225
 Asp Gln Trp Val Gln Asp Lys Ile Thr Gln Met Lys Tyr Val Thr
 230 235 240
 Asp Val Gly Val Leu Gln Arg His Val Ser Arg His Asn His Arg

Asn Glu Asp Glu	245	Val Asp Cys Thr Arg	250	Ile	255
Glu Asn Thr Leu Ser	260	Leu Tyr Gln His Trp	265	Ser	270
Ser Phe Glu Tyr	275	Leu Arg Leu Val	280	Ser	285
Leu His Asp Ser	290	Tyr Thr Ala Ala Arg	295	Phe	300
Lys Leu Trp Ser	305	Val His Gly Gln Lys	310	Phe	315
Ala Asp Met Gly	320	Val Lys Gln Lys Phe	325	Gln	330
Ala Met Asp Ile	335	Leu Arg Glu Met Ile	340	Glu	345
Glu Ser Ala Asn	350	Asp Met Arg Val Gln	355	Thr	360
Phe Ser Ile His	365	Lys Phe Leu Ala Ser	370	Asp	375
Val Val Phe Ala	380	Glu Ser Pro Glu Lys	385	Asp	390
Gly Ser Gly Thr	395	Ala Leu Asp Ser Leu	400	Ser	405
Arg Ser Asn Leu	410	Gly Leu Glu Leu Ala	415	Lys	420
Lys Gln Leu Arg	425	Ile Ala Ser Cys Leu	430	Cys	435
Thr Asn Leu Val	440	Phe Leu Tyr Cys Ser	445	Leu	450
Met Glu Gly Thr	455	Phe Ser Arg Pro Ala	460	Ser	465
Leu Ser Leu Leu	470	Lys Ser Phe Val Cys	475	Ser	480
Thr Lys Asn Arg	485	Pro Leu Val Met Ala	490	Ala	495
Pro Leu Ser Met	500	Thr Val Val Gly Ile	505	Pro	510
Pro Glu Thr Asp	515	Asn Phe Phe Gly Arg	520	Ala	525
Phe Glu Lys Ala	530	Ser Arg Met Leu His	535	Asn	540
His Phe Asp Leu	545	Lys Ala Glu Asp Arg	550	Ser	555
Lys Phe Leu Asp	Ala	Leu Ile Ser Leu	Leu	Ser	

<210> 42
 <211> 380
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 44, 118, 172, 183
 <223> unknown base

<400> 42
 gtacctcagc gcgagcgcca ggcgtccggc cgccgtggct atgntcgtgt 50
 ccgatttccg caaagagttc tacgaggtgg tccagagcca gagggtcctt 100
 ctcttcgtgg cctcggangt ggatgctctg tgtgcgtgca agatccttca 150
 ggccttggtc cagtgtgacc angtgcaata tangctgggt ccagtttctg 200
 ggtggcaaga acttgaaact gcatttcttg agcataaaga acagtttcat 250
 tattttattc tcataaactg tggagctaag gtagacctat tggatattct 300
 tcaacctgat gaagacacta tattctttgt gtgtgacacc cataggccag 350
 tcaatgttgt caatgtatac aacgataccc 380

<210> 43
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 43
 ttccgcaaag agttctacga ggtgg 25

<210> 44
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 44
 attgacaaca ttgactggcc tatggg 26

<210> 45
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 45
 gtggatgctc tgtgtgcgtg caagatcctt caggccttgt tccagtgtga 50

<210> 46

<211> 3089
 <212> DNA
 <213> Homo sapiens

<400> 46
 caggaaccct ctctttgggt ctggattggg acccctttcc agtaccattt 50
 tttctagtga accacgaagg gacgatacca gaaaacaccc tcaacccaaa 100
 ggaaatagac tacagcccca attggctgac tttggctata gaaaaaagaa 150
 aggaacgaaa agagacagtt ttttttgaa agctaagtct tccctttatc 200
 gagtcaagaa accccccctt cttgagctat ttacagcttt taacaattga 250
 gtaaagtacg ctccggtcac catggtgaca gccgccctgg gtcccgtctg 300
 ggcagcgctc ctgctctttc tctgatgtg tgagatccgt atggtggagc 350
 tcacctttga cagagctgtg gccagcggct gccaacggtg ctgtgactct 400
 gaggaccccc tggatcctgc ccatgtatcc tcagcctctt cctccggccg 450
 cccccacgcc ctgcctgaga tcagacccta cattaatatc accatcctga 500
 agggtgacaa aggggaccca ggcccaatgg gcctgccagg gtacatgggc 550
 agggaggggtc cccaagggga gcctggccct cagggcagca agggtgacaa 600
 gggggagatg ggcagccccg gcgccccgtg ccagaagcgc ttcttcgcct 650
 tctcagtggg ccgcaagacg gccctgcaca gcggcgagga cttccagacg 700
 ctgctcttcg aaagggctct tgtgaacctt gatgggtgct ttgacatggc 750
 gaccggccag tttgctgctc ccctgcgtgg catctacttc ttcagcctca 800
 atgtgcacag ctggaattac aaggagacgt acgtgcacat tatgcataac 850
 cagaaagagg ctgtcatcct gtacgcgcag ccagcgcagc gcagcatcat 900
 gcagagccag agtgtgatgc tggacctggc ctacggggac cgcgtctggg 950
 tgcggctctt caagcgccag cgcgagaacg ccatctacag caacgacttc 1000
 gacacctaca tcaccttcag cggccacctc atcaaggccg aggacgactg 1050
 agggcctctg ggccaccctc ccggtggag agctcaggtg ctggtcccgt 1100
 cccctgcagg gctcagtttg cactgctgtg aagcaggaag gccagggagg 1150
 tccccgggga cctggcattc tggggagacc ctgcttctat cttggctgcc 1200
 atcatccctc ccagcctatt tctgctctc tcttctctct tggacctatt 1250
 ttaagaagct tgctaacct aatattctag aactttcca gcctcgtagc 1300
 ccagcacttc tcaaacttgg aaatgcatgc gaatcaccgc gggttcgtgt 1350
 taaatgcaga ttctgactca gcaggtctga gtgggtccag gattctgtgt 1400
 ttctcatatg ttctgggtg atgctgatgg ggtcagtcta tgaaccacac 1450

tggagcaacc aggttctagg acttttctcaa tattctagta ctttctgaac 1500
 attctggaat cctccccaca ttctagaatt ctccaacat ttttttttct 1550
 tgagacagag tcttgctctg ttgcccaggc tagagtgcag tgggtgcaatc 1600
 tcagttcact gcaacctctg cctcccgggt tcaagcgatt cttctgcctc 1650
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 cttgaactcc tgacttcagg tgaccacccc gcctcggcct ctcaaaatgc 1800
 tgggattaca ggtgtgagcc accgtgcctg gccaatcca acattcttaa 1850
 attctctcat ccctccaggg ctccccgtgc tatgttctct ttacccttc 1900
 cccctcttct cttgctcagg cctgcaccac tgcagccacc gttcatttat 1950
 tcattcatta aacactgagc actcactctg tgctgggtcc cgggaagggt 2000
 gaggggggtca gacacaggcc ctgcccctgc cctcagtgc tggccagtcc 2050
 agcccaggcg gggagagatg tgtacatagg ttttaaagca gaccagagc 2100
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 ccaactgctcc ccaaggctgg tgggacgggg tcccgggtggc aggggcaggt 2200
 atctccttcc cgttctcat ccacctgcc agtgctcatc gttacagcaa 2250
 accccagggg gccttgcca ggtcaagggt tctgtgagga gaggaccag 2300
 gagtgtgggg gcatttgggg ggtgaagtgg ccccgaaga atggaacca 2350
 caccatagc tctccccaca gctgatacgg catcctgcga gaagacctgc 2400
 cctcctcact gggatccct tctgcctcc tcccagggt ctgccagggc 2450
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<211> 673

<212> PRT

<213> Homo sapiens

<400> 52

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Ser	Gln	Pro	Gln	Thr	Val	Phe	Cys	Thr	Ala	Arg	Gln	Gly	Thr	Thr
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Val	Pro	Arg	Asp	Val	Pro	Pro	Asp	Thr	Val	Gly	Leu	Tyr	Val	Phe
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Glu	Asn	Gly	Ile	Thr	Met	Leu	Asp	Ala	Gly	Ser	Phe	Ala	Gly	Leu
				65					70					75
Pro	Gly	Leu	Gln	Leu	Leu	Asp	Leu	Ser	Gln	Asn	Gln	Ile	Ala	Ser
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Leu	Pro	Ser	Gly	Val	Phe	Gln	Pro	Leu	Ala	Asn	Leu	Ser	Asn	Leu

				95					100					105
Asp	Leu	Thr	Ala	Asn 110	Arg	Leu	His	Glu	Ile 115	Thr	Asn	Glu	Thr	Phe 120
Arg	Gly	Leu	Arg	Arg 125	Leu	Glu	Arg	Leu	Tyr 130	Leu	Gly	Lys	Asn	Arg 135
Ile	Arg	His	Ile	Gln 140	Pro	Gly	Ala	Phe	Asp 145	Thr	Leu	Asp	Arg	Leu 150
Leu	Glu	Leu	Lys	Leu 155	Gln	Asp	Asn	Glu	Leu 160	Arg	Ala	Leu	Pro	Pro 165
Leu	Arg	Leu	Pro	Arg 170	Leu	Leu	Leu	Leu	Asp 175	Leu	Ser	His	Asn	Ser 180
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Ala	Leu	Arg	Leu	Ala 200	Gly	Leu	Gly	Leu	Gln 205	Gln	Leu	Asp	Glu	Gly 210
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Arg	Pro	Glu	Asp	Leu 260	Ala	Gly	Leu	Ala	Ala 265	Leu	Gln	Glu	Leu	Asp 270
Val	Ser	Asn	Leu	Ser 275	Leu	Gln	Ala	Leu	Pro 280	Gly	Asp	Leu	Ser	Gly 285
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Ser	His	Val	Thr	Leu 320	Ala	Ser	Pro	Glu	Glu 325	Thr	Arg	Cys	His	Phe 330
Pro	Pro	Lys	Asn	Ala 335	Gly	Arg	Leu	Leu	Leu 340	Glu	Leu	Asp	Tyr	Ala 345
Asp	Phe	Gly	Cys	Pro 350	Ala	Thr	Thr	Thr	Thr 355	Ala	Thr	Val	Pro	Thr 360
Thr	Arg	Pro	Val	Val 365	Arg	Glu	Pro	Thr	Ala 370	Leu	Ser	Ser	Ser	Leu 375
Ala	Pro	Thr	Trp	Leu 380	Ser	Pro	Thr	Ala	Pro 385	Ala	Thr	Glu	Ala	Pro 390
Ser	Pro	Pro	Ser	Thr 395	Ala	Pro	Pro	Thr	Val 400	Gly	Pro	Val	Pro	Gln 405
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Phe Thr Gly Leu Tyr Cys Glu Ser Gln Met Gly Gln Gly Thr Arg		
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Pro Ser Pro Thr Pro Val Thr Pro Arg Pro Pro Arg Ser Leu Thr		
455	460	465
Leu Gly Ile Glu Pro Val Ser Pro Thr Ser Leu Arg Val Gly Leu		
470	475	480
Gln Arg Tyr Leu Gln Gly Ser Ser Val Gln Leu Arg Ser Leu Arg		
485	490	495
Leu Thr Tyr Arg Asn Leu Ser Gly Pro Asp Lys Arg Leu Val Thr		
500	505	510
Leu Arg Leu Pro Ala Ser Leu Ala Glu Tyr Thr Val Thr Gln Leu		
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Arg Pro Asn Ala Thr Tyr Ser Val Cys Val Met Pro Leu Gly Pro		
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Gly Arg Val Pro Glu Gly Glu Glu Ala Cys Gly Glu Ala His Thr		
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Pro Pro Ala Val His Ser Asn His Ala Pro Val Thr Gln Ala Arg		
560	565	570
Glu Gly Asn Leu Pro Leu Leu Ile Ala Pro Ala Leu Ala Ala Val		
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Leu Leu Ala Ala Leu Ala Ala Val Gly Ala Ala Tyr Cys Val Arg		
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Arg Gly Arg Ala Met Ala Ala Ala Ala Gln Asp Lys Gly Gln Val		
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Gly Pro Gly Ala Gly Pro Leu Glu Leu Glu Gly Val Lys Val Pro		
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Leu Glu Pro Gly Pro Lys Ala Thr Glu Gly Gly Gly Glu Ala Leu		
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<211> 811
<212> PRT
<213> Homo sapiens

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35 40 45
Leu Thr Pro Ala Thr Thr Thr Leu Asp Leu Ser Tyr Asn Leu Leu 60
50 55 60
Phe Gln Leu Gln Ser Ser Asp Phe His Ser Val Ser Lys Leu Arg 75
65 70 75
Val Leu Ile Leu Cys His Asn Arg Ile Gln Gln Leu Asp Leu Lys 90
80 85 90

Thr	Phe	Glu	Phe	Asn	Lys	Glu	Leu	Arg	Tyr	Leu	Asp	Leu	Ser	Asn	
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Asn	Arg	Leu	Lys	Ser	Val	Thr	Trp	Tyr	Leu	Leu	Ala	Gly	Leu	Arg	
				110					115					120	
Tyr	Leu	Asp	Leu	Ser	Phe	Asn	Asp	Phe	Asp	Thr	Met	Pro	Ile	Cys	
				125					130					135	
Glu	Glu	Ala	Gly	Asn	Met	Ser	His	Leu	Glu	Ile	Leu	Gly	Leu	Ser	
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Gly	Ala	Lys	Ile	Gln	Lys	Ser	Asp	Phe	Gln	Lys	Ile	Ala	His	Leu	
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His	Leu	Asn	Thr	Val	Phe	Leu	Gly	Phe	Arg	Thr	Leu	Pro	His	Tyr	
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Glu	Glu	Gly	Ser	Leu	Pro	Ile	Leu	Asn	Thr	Thr	Lys	Leu	His	Ile	
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Val	Leu	Pro	Met	Asp	Thr	Asn	Phe	Trp	Val	Leu	Leu	Arg	Asp	Gly	
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Ile	Lys	Thr	Ser	Lys	Ile	Leu	Glu	Met	Thr	Asn	Ile	Asp	Gly	Lys	
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Ser	Gln	Phe	Val	Ser	Tyr	Glu	Met	Gln	Arg	Asn	Leu	Ser	Leu	Glu	
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Asn	Ala	Lys	Thr	Ser	Val	Leu	Leu	Leu	Asn	Lys	Val	Asp	Leu	Leu	
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Trp	Asp	Asp	Leu	Phe	Leu	Ile	Leu	Gln	Phe	Val	Trp	His	Thr	Ser	
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Val	Glu	His	Phe	Gln	Ile	Arg	Asn	Val	Thr	Phe	Gly	Gly	Lys	Ala	
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Tyr	Leu	Asp	His	Asn	Ser	Phe	Asp	Tyr	Ser	Asn	Thr	Val	Met	Arg	
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Thr	Ile	Lys	Leu	Glu	His	Val	His	Phe	Arg	Val	Phe	Tyr	Ile	Gln	
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Gln	Asp	Lys	Ile	Tyr	Leu	Leu	Leu	Thr	Lys	Met	Asp	Ile	Glu	Asn	
				320					325					330	
Leu	Thr	Ile	Ser	Asn	Ala	Gln	Met	Pro	His	Met	Leu	Phe	Pro	Asn	
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Tyr	Pro	Thr	Lys	Phe	Gln	Tyr	Leu	Asn	Phe	Ala	Asn	Asn	Ile	Leu	
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Thr	Asp	Glu	Leu	Phe	Lys	Arg	Thr	Ile	Gln	Leu	Pro	His	Leu	Lys	
				365					370					375	
Thr	Leu	Ile	Leu	Asn	Gly	Asn	Lys	Leu	Glu	Thr	Leu	Ser	Leu	Val	
				380					385					390	
Ser	Cys	Phe	Ala	Asn	Asn	Thr	Pro	Leu	Glu	His	Leu	Asp	Leu	Ser	
				395					400					405	

Gln	Asn	Leu	Leu	Gln	His	Lys	Asn	Asp	Glu	Asn	Cys	Ser	Trp	Pro	410	415	420
Glu	Thr	Val	Val	Asn	Met	Asn	Leu	Ser	Tyr	Asn	Lys	Leu	Ser	Asp	425	430	435
Ser	Val	Phe	Arg	Cys	Leu	Pro	Lys	Ser	Ile	Gln	Ile	Leu	Asp	Leu	440	445	450
Asn	Asn	Asn	Gln	Ile	Gln	Thr	Val	Pro	Lys	Glu	Thr	Ile	His	Leu	455	460	465
Met	Ala	Leu	Arg	Glu	Leu	Asn	Ile	Ala	Phe	Asn	Phe	Leu	Thr	Asp	470	475	480
Leu	Pro	Gly	Cys	Ser	His	Phe	Ser	Arg	Leu	Ser	Val	Leu	Asn	Ile	485	490	495
Glu	Met	Asn	Phe	Ile	Leu	Ser	Pro	Ser	Leu	Asp	Phe	Val	Gln	Ser	500	505	510
Cys	Gln	Glu	Val	Lys	Thr	Leu	Asn	Ala	Gly	Arg	Asn	Pro	Phe	Arg	515	520	525
Cys	Thr	Cys	Glu	Leu	Lys	Asn	Phe	Ile	Gln	Leu	Glu	Thr	Tyr	Ser	530	535	540
Glu	Val	Met	Met	Val	Gly	Trp	Ser	Asp	Ser	Tyr	Thr	Cys	Glu	Tyr	545	550	555
Pro	Leu	Asn	Leu	Arg	Gly	Thr	Arg	Leu	Lys	Asp	Val	His	Leu	His	560	565	570
Glu	Leu	Ser	Cys	Asn	Thr	Ala	Leu	Leu	Ile	Val	Thr	Ile	Val	Val	575	580	585
Ile	Met	Leu	Val	Leu	Gly	Leu	Ala	Val	Ala	Phe	Cys	Cys	Leu	His	590	595	600
Phe	Asp	Leu	Pro	Trp	Tyr	Leu	Arg	Met	Leu	Gly	Gln	Cys	Thr	Gln	605	610	615
Thr	Trp	His	Arg	Val	Arg	Lys	Thr	Thr	Gln	Glu	Gln	Leu	Lys	Arg	620	625	630
Asn	Val	Arg	Phe	His	Ala	Phe	Ile	Ser	Tyr	Ser	Glu	His	Asp	Ser	635	640	645
Leu	Trp	Val	Lys	Asn	Glu	Leu	Ile	Pro	Asn	Leu	Glu	Lys	Glu	Asp	650	655	660
Gly	Ser	Ile	Leu	Ile	Cys	Leu	Tyr	Glu	Ser	Tyr	Phe	Asp	Pro	Gly	665	670	675
Lys	Ser	Ile	Ser	Glu	Asn	Ile	Val	Ser	Phe	Ile	Glu	Lys	Ser	Tyr	680	685	690
Lys	Ser	Ile	Phe	Val	Leu	Ser	Pro	Asn	Phe	Val	Gln	Asn	Glu	Trp	695	700	705
Cys	His	Tyr	Glu	Phe	Tyr	Phe	Ala	His	His	Asn	Leu	Phe	His	Glu	710	715	720

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Glu	Val	Asp	Ala	Arg 200	Arg	Leu	Thr	Arg	Phe 205	Thr	Gly	Val	Ile	Thr 210
Gln	Gly	Arg	Asn	Ser 215	Leu	Trp	Leu	Ser	Asp 220	Trp	Val	Thr	Ser	Tyr 225
Lys	Val	Met	Val	Ser 230	Asn	Asp	Ser	His	Thr 235	Trp	Val	Thr	Val	Lys 240
Asn	Gly	Ser	Gly	Asp 245	Met	Ile	Phe	Glu	Gly 250	Asn	Ser	Glu	Lys	Glu 255
Ile	Pro	Val	Leu	Asn 260	Glu	Leu	Pro	Val	Pro 265	Met	Val	Ala	Arg	Tyr 270
Ile	Arg	Ile	Asn	Pro 275	Gln	Ser	Trp	Phe	Asp 280	Asn	Gly	Ser	Ile	Cys 285
Met	Arg	Met	Glu	Ile 290	Leu	Gly	Cys	Pro	Leu 295	Pro	Asp	Pro	Asn	Asn 300
Tyr	Tyr	His	Arg	Arg 305	Asn	Glu	Met	Thr	Thr 310	Thr	Asp	Asp	Leu	Asp 315
Phe	Lys	His	His	Asn 320	Tyr	Lys	Glu	Met	Arg 325	Gln	Leu	Met	Lys	Val 330
Val	Asn	Glu	Met	Cys 335	Pro	Asn	Ile	Thr	Arg 340	Ile	Tyr	Asn	Ile	Gly 345
Lys	Ser	His	Gln	Gly 350	Leu	Lys	Leu	Tyr	Ala 355	Val	Glu	Ile	Ser	Asp 360
His	Pro	Gly	Glu	His 365	Glu	Val	Gly	Glu	Pro 370	Glu	Phe	His	Tyr	Ile 375
Ala	Gly	Ala	His	Gly 380	Asn	Glu	Val	Leu	Gly 385	Arg	Glu	Leu	Leu	Leu 390
Leu	Leu	Val	Gln	Phe 395	Val	Cys	Gln	Glu	Tyr 400	Leu	Ala	Arg	Asn	Ala 405
Arg	Ile	Val	His	Leu 410	Val	Glu	Glu	Thr	Arg 415	Ile	His	Val	Leu	Pro 420
Ser	Leu	Asn	Pro	Asp 425	Gly	Tyr	Glu	Lys	Ala 430	Tyr	Glu	Gly	Gly	Ser 435
Glu	Leu	Gly	Gly	Trp 440	Ser	Leu	Gly	Arg	Trp 445	Thr	His	Asp	Gly	Ile 450
Asp	Ile	Asn	Asn	Asn 455	Phe	Pro	Asp	Leu	Asn 460	Thr	Leu	Leu	Trp	Glu 465
Ala	Glu	Asp	Arg	Gln 470	Asn	Val	Pro	Arg	Lys 475	Val	Pro	Asn	His	Tyr 480
Ile	Ala	Ile	Pro	Glu 485	Trp	Phe	Leu	Ser	Glu 490	Asn	Ala	Thr	Val	Ala 495
Ala	Glu	Thr	Arg	Ala	Val	Ile	Ala	Trp	Met	Glu	Lys	Ile	Pro	Phe

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Val Leu Gly Gly Asn Leu Gln Gly Gly 515	Glu Leu Val Val Ala Tyr 520	
Pro Tyr Asp Leu Val Arg Ser Pro Trp 530	Lys Thr Gln Glu His Thr 535	
Pro Thr Pro Asp Asp His Val Phe Arg 545	Trp Leu Ala Tyr Ser Tyr 550	
Ala Ser Thr His Arg Leu Met Thr Asp 560	Ala Arg Arg Arg Val Cys 565	
His Thr Glu Asp Phe Gln Lys Glu Glu 575	Gly Thr Val Asn Gly Ala 580	
Ser Trp His Thr Val Ala Gly Ser Leu 590	Asn Asp Phe Ser Tyr Leu 595	
His Thr Asn Cys Phe Glu Leu Ser Ile 605	Tyr Val Gly Cys Asp Lys 610	
Tyr Pro His Glu Ser Gln Leu Pro Glu 620	Glu Trp Glu Asn Asn Arg 625	
Glu Ser Leu Ile Val Phe Met Glu Gln 635	Val His Arg Gly Ile Lys 640	
Gly Leu Val Arg Asp Ser His Gly Lys 650	Gly Ile Pro Asn Ala Ile 655	
Ile Ser Val Glu Gly Ile Asn His Asp 665	Ile Arg Thr Ala Asn Asp 670	
Gly Asp Tyr Trp Arg Leu Leu Asn Pro 680	Gly Glu Tyr Val Val Thr 685	
Ala Lys Ala Glu Gly Phe Thr Ala Ser 695	Thr Lys Asn Cys Met Val 700	
Gly Tyr Asp Met Gly Ala Thr Arg Cys 710	Asp Phe Thr Leu Ser Lys 715	
Thr Asn Met Ala Arg Ile Arg Glu Ile 725	Met Glu Lys Phe Gly Lys 730	
Gln Pro Val Ser Leu Pro Ala Arg Arg 740	Leu Lys Leu Arg Gly Arg 745	
Lys Arg Arg Gln Arg Gly 755		

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<211> 24

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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 63

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<210> 64
<211> 24
<212> DNA
<213> Artificial Sequence

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<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 66
<211> 2854
<212> DNA
<213> Homo sapiens

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cccagccccg gcttcagctc tttcccaggt gttgactcca gctccagctt 150
cagctccagc tccaggtcgg gctccagctc cagccgcagc ttaggcagcg 200
gaggttctgt gtcccagttg ttttccaatt tcaccggctc cgtggatgac 250
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aaaa 2854

<210> 67
<211> 510
<212> PRT
<213> Homo sapiens

<400> 67
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Ser Pro Gly Phe Ser Ser Phe Pro Gly Val Asp Ser Ser Ser Ser
35 40 45
Phe Ser Ser Ser Ser Arg Ser Gly Ser Ser Ser Ser Arg Ser Leu
50 55 60
Gly Ser Gly Gly Ser Val Ser Gln Leu Phe Ser Asn Phe Thr Gly
65 70 75
Ser Val Asp Asp Arg Gly Thr Cys Gln Cys Ser Val Ser Leu Pro
80 85 90
Asp Thr Thr Phe Pro Val Asp Arg Val Glu Arg Leu Glu Phe Thr
95 100 105
Ala His Val Leu Ser Gln Lys Phe Glu Lys Glu Leu Ser Lys Val
110 115 120
Arg Glu Tyr Val Gln Leu Ile Ser Val Tyr Glu Lys Lys Leu Leu
125 130 135
Asn Leu Thr Val Arg Ile Asp Ile Met Glu Lys Asp Thr Ile Ser
140 145 150
Tyr Thr Glu Leu Asp Phe Glu Leu Ile Lys Val Glu Val Lys Glu
155 160 165
Met Glu Lys Leu Val Ile Gln Leu Lys Glu Ser Phe Gly Gly Ser
170 175 180
Ser Glu Ile Val Asp Gln Leu Glu Val Glu Ile Arg Asn Met Thr
185 190 195
Leu Leu Val Glu Lys Leu Glu Thr Leu Asp Lys Asn Asn Val Leu
200 205 210

Ala	Ile	Arg	Arg	Glu	Ile	Val	Ala	Leu	Lys	Thr	Lys	Leu	Lys	Glu	215	220	225
Cys	Glu	Ala	Ser	Lys	Asp	Gln	Asn	Thr	Pro	Val	Val	His	Pro	Pro	230	235	240
Pro	Thr	Pro	Gly	Ser	Cys	Gly	His	Gly	Gly	Val	Val	Asn	Ile	Ser	245	250	255
Lys	Pro	Ser	Val	Val	Gln	Leu	Asn	Trp	Arg	Gly	Phe	Ser	Tyr	Leu	260	265	270
Tyr	Gly	Ala	Trp	Gly	Arg	Asp	Tyr	Ser	Pro	Gln	His	Pro	Asn	Lys	275	280	285
Gly	Leu	Tyr	Trp	Val	Ala	Pro	Leu	Asn	Thr	Asp	Gly	Arg	Leu	Leu	290	295	300
Glu	Tyr	Tyr	Arg	Leu	Tyr	Asn	Thr	Leu	Asp	Asp	Leu	Leu	Leu	Tyr	305	310	315
Ile	Asn	Ala	Arg	Glu	Leu	Arg	Ile	Thr	Tyr	Gly	Gln	Gly	Ser	Gly	320	325	330
Thr	Ala	Val	Tyr	Asn	Asn	Asn	Met	Tyr	Val	Asn	Met	Tyr	Asn	Thr	335	340	345
Gly	Asn	Ile	Ala	Arg	Val	Asn	Leu	Thr	Thr	Asn	Thr	Ile	Ala	Val	350	355	360
Thr	Gln	Thr	Leu	Pro	Asn	Ala	Ala	Tyr	Asn	Asn	Arg	Phe	Ser	Tyr	365	370	375
Ala	Asn	Val	Ala	Trp	Gln	Asp	Ile	Asp	Phe	Ala	Val	Asp	Glu	Asn	380	385	390
Gly	Leu	Trp	Val	Ile	Tyr	Ser	Thr	Glu	Ala	Ser	Thr	Gly	Asn	Met	395	400	405
Val	Ile	Ser	Lys	Leu	Asn	Asp	Thr	Thr	Leu	Gln	Val	Leu	Asn	Thr	410	415	420
Trp	Tyr	Thr	Lys	Gln	Tyr	Lys	Pro	Ser	Ala	Ser	Asn	Ala	Phe	Met	425	430	435
Val	Cys	Gly	Val	Leu	Tyr	Ala	Thr	Arg	Thr	Met	Asn	Thr	Arg	Thr	440	445	450
Glu	Glu	Ile	Phe	Tyr	Tyr	Tyr	Asp	Thr	Asn	Thr	Gly	Lys	Glu	Gly	455	460	465
Lys	Leu	Asp	Ile	Val	Met	His	Lys	Met	Gln	Glu	Lys	Val	Gln	Ser	470	475	480
Ile	Asn	Tyr	Asn	Pro	Phe	Asp	Gln	Lys	Leu	Tyr	Val	Tyr	Asn	Asp	485	490	495
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<210> 68
 <211> 410
 <212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 206, 217, 387

<223> unknown base

<400> 68

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taacctgacc 410

<210> 69

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 69

agctgtggtc atggtggtgt ggtg 24

<210> 70

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 70

ctaccttggc cataggtgat ccgc 24

<210> 71

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 71

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<210> 72

<211> 3127

<212> DNA

<213> Homo sapiens

<400> 72

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tggggctgtg ctccatggcg agctggatac catgtttgtg tggaagtgcc 150
ccgtgtttgc tatgccgatg ctgtcctagt ggaaacaact ccaactgtaac 200
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<210> 73
 <211> 453
 <212> PRT
 <213> Homo sapiens

<400> 73

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Ser	Gly	Asn	Asn	Ser	Thr	Val	Thr	Arg	Leu	Ile	Tyr	Ala	Leu	Phe	
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Leu	Leu	Val	Gly	Val	Cys	Val	Ala	Cys	Val	Met	Leu	Ile	Pro	Gly	
				50					55					60	
Met	Glu	Glu	Gln	Leu	Asn	Lys	Ile	Pro	Gly	Phe	Cys	Glu	Asn	Glu	
				65					70					75	
Lys	Gly	Val	Val	Pro	Cys	Asn	Ile	Leu	Val	Gly	Tyr	Lys	Ala	Val	
				80					85					90	
Tyr	Arg	Leu	Cys	Phe	Gly	Leu	Ala	Met	Phe	Tyr	Leu	Leu	Leu	Ser	
				95					100					105	
Leu	Leu	Met	Ile	Lys	Val	Lys	Ser	Ser	Ser	Asp	Pro	Arg	Ala	Ala	
				110					115					120	
Val	His	Asn	Gly	Phe	Trp	Phe	Phe	Lys	Phe	Ala	Ala	Ala	Ile	Ala	
				125					130					135	
Ile	Ile	Ile	Gly	Ala	Phe	Phe	Ile	Pro	Glu	Gly	Thr	Phe	Thr	Thr	
				140					145					150	
Val	Trp	Phe	Tyr	Val	Gly	Met	Ala	Gly	Ala	Phe	Cys	Phe	Ile	Leu	
				155					160					165	
Ile	Gln	Leu	Val	Leu	Leu	Ile	Asp	Phe	Ala	His	Ser	Trp	Asn	Glu	
				170					175					180	
Ser	Trp	Val	Glu	Lys	Met	Glu	Glu	Gly	Asn	Ser	Arg	Cys	Trp	Tyr	
				185					190					195	
Ala	Ala	Leu	Leu	Ser	Ala	Thr	Ala	Leu	Asn	Tyr	Leu	Leu	Ser	Leu	
				200					205					210	
Val	Ala	Ile	Val	Leu	Phe	Phe	Val	Tyr	Tyr	Thr	His	Pro	Ala	Ser	
				215					220					225	
Cys	Ser	Glu	Asn	Lys	Ala	Phe	Ile	Ser	Val	Asn	Met	Leu	Leu	Cys	
				230					235					240	
Val	Gly	Ala	Ser	Val	Met	Ser	Ile	Leu	Pro	Lys	Ile	Gln	Glu	Ser	
				245					250					255	
Gln	Pro	Arg	Ser	Gly	Leu	Leu	Gln	Ser	Ser	Val	Ile	Thr	Val	Tyr	
				260					265					270	
Thr	Met	Tyr	Leu	Thr	Trp	Ser	Ala	Met	Thr	Asn	Glu	Pro	Glu	Thr	
				275					280					285	

Asn	Cys	Asn	Pro	Ser	Leu	Leu	Ser	Ile	Ile	Gly	Tyr	Asn	Thr	Thr	
				290					295					300	
Ser	Thr	Val	Pro	Lys	Glu	Gly	Gln	Ser	Val	Gln	Trp	Trp	His	Ala	
				305					310					315	
Gln	Gly	Ile	Ile	Gly	Leu	Ile	Leu	Phe	Leu	Leu	Cys	Val	Phe	Tyr	
				320					325					330	
Ser	Ser	Ile	Arg	Thr	Ser	Asn	Asn	Ser	Gln	Val	Asn	Lys	Leu	Thr	
				335					340					345	
Leu	Thr	Ser	Asp	Glu	Ser	Thr	Leu	Ile	Glu	Asp	Gly	Gly	Ala	Arg	
				350					355					360	
Ser	Asp	Gly	Ser	Leu	Glu	Asp	Gly	Asp	Asp	Val	His	Arg	Ala	Val	
				365					370					375	
Asp	Asn	Glu	Arg	Asp	Gly	Val	Thr	Tyr	Ser	Tyr	Ser	Phe	Phe	His	
				380					385					390	
Phe	Met	Leu	Phe	Leu	Ala	Ser	Leu	Tyr	Ile	Met	Met	Thr	Leu	Thr	
				395					400					405	
Asn	Trp	Ser	Arg	Tyr	Glu	Pro	Ser	Arg	Glu	Met	Lys	Ser	Gln	Trp	
				410					415					420	
Thr	Ala	Val	Trp	Val	Lys	Ile	Ser	Ser	Ser	Trp	Ile	Gly	Ile	Val	
				425					430					435	
Leu	Tyr	Val	Trp	Thr	Leu	Val	Ala	Pro	Leu	Val	Leu	Thr	Asn	Arg	
				440					445					450	

Asp Phe Asp

<210> 74
 <211> 480
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 48, 163
 <223> unknown base

<400> 74
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 cgttgtggag atggggagcg tccttggggc tgtgtccat ggcgagctgg 100
 ataccatggt tgtgtggaag tgccccgtgt ttgctatgcc gatgctgtcc 150
 tagtggaac aantccactg taactagatt gatctatgca cttttcttgc 200
 ttgttgagat atgtgtagct tgtgtaatgt tgataccagg aatggaagaa 250
 caactgaata agattcctgg attttgtgag aatgagaaag gtgttgtccc 300
 ttgtaacatt ttggttggt ataaagctgt atatcgtttg tgctttggtt 350
 tggctatggt ctatcttctt ctctctttac taatgatcaa agtgaagagt 400

agcagtgatc ctagagctgc agtgcacaat ggatttttggg tcttttaaatt 450
tgctgcagca attgcaatta ttattggggc 480

<210> 75
<211> 438
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 32, 65, 92, 121, 142, 154, 170, 293, 315, 323
<223> unknown base

<400> 75
gttattgtga actttgtgga gatgggaggt cntggggctg tgttccatgg 50
cgagctggat accangtttg tgtggaagtg ccccggtgtt gntatgccga 100
tgctgtccta gtggaaacaa ntccactgta attagattga tntatgcact 150
tttnttgctt gttggagtan gtgtagcttg tgtaatgttg ataccaggaa 200
tggaagaaca actgaataag attcctggat tttgtgagaa tgagaaaggt 250
gttgtccctt gtaacatddd ggttggctat aaagctgtat atngtttgtg 300
ctttggtttg gctangttct atnttcttct ctctttacta atgatcaaag 350
tgaagagtag cagtgatcct agagctgcag tgcacaatgg attttggttt 400
tttaaatttg ctgcagcaat tgcaattatt attggggc 438

<210> 76
<211> 473
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 48
<223> unknown base

<400> 76
aagaagctgt ctccatcttg totgtatccg ctgctcttgt gaacgttntg 50
gagatgggga gcgtccttgg ggttgtgctc catggcgagc tggataccat 100
gtttgtgtgg aagtgtcccg tgtttgctat gccgatgctg tcctagtggg 150
aacaactcca ctgtaactag attgatctat gcacttttct tgcttggttg 200
agtatgtgta gcttgtgtaa tgttgatacc aggaatggaa gaacaactga 250
ataagattcc tggattttgt gagaatgaga aagggtgttg cocttgtaac 300
attttggttg gctataaagc tgtatatcgt ttgtgctttg gtttggctat 350
gttctatctt cttctctctt tactaatgat caaagtgaag agtagcagtg 400
atcctagagc tgcagtgcac aatggatttt ggttctttta atttgctgca 450
gcaattgcaa ttattatttg ggc 473

<210> 77
<211> 666
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 21, 111
<223> unknown base

<400> 77
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actttttcct tgcttggttg agtatgtgta gctttgtgta atgttgttcc 100
caggattgga ngaacaactg aataagattc ctggattttt gtgagaatga 150
gaaaggtggt gtcccccttg aacatttttg gttggctata aagctgtata 200
tcgtttgtgc ttggttttg ctatgttcta tcttcttctc tctttactaa 250
tgatcaaagt gaagagtagc agtgatccta gagctgcagt gcacaatgga 300
ttttggttct ttaaatttgc tgcagcaatt gcaattatta ttggggcatt 350
cttcattcca gaaggaactt ttacaactgt gtggttttat gtaggcattg 400
cagggtgcctt ttgtttcatc ctcatacaac tagtcttact tattgatttt 450
gcacattcat ggaatgaatc gtgggttgaa aaaatggaag aagggaactc 500
gagatgttgg tatgcagcct tggtatcagc tacagctctg aattatctgc 550
tgtctttagt tgctatcgtc ctgttctttg tctactacac tcatccagcc 600
agttgttcag aaaacaaggc gttcatcagt gtcaacatgc tcctctgcgt 650
tggtgcttct gtaatg 666

<210> 78
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 78
atgtttgtgt ggaagtgcc cg 22

<210> 79
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 79
gtcaacatgc tcctctgc 18

<210> 80
<211> 26

<212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 80
 aatccattgt gactgcagc tctagg 26

<210> 81
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 81
 gagcatgcc ccaactggact gac 23

<210> 82
 <211> 54
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 82
 gccgatgctg tcctagtggg aacaactcca ctgtaactag attgatctat 50

gcac 54

<210> 83
 <211> 3906
 <212> DNA
 <213> Homo sapiens

<400> 83
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 gcgggccggcg ccggcctctc caatggcaaa tgtgtgtggc tggaggcgag 100
 cgcgaggctt tcggcaaagg cagtcgagtg tttgcagacc ggggagagtc 150
 ctgtgaaagc agataaaaga aaacatttat taacgtgtca ttacgagggg 200
 agcgcccgcg cggggctgtc gcaactcccc cggaacattt ggctccctcc 250
 agctccgaga gaggagaaga agaaagcgga aaagaggcag attcacgtcg 300
 tttccagcca agtggacctg atcgatggcc ctctgaatt tatcacgata 350
 tttgatttat tagcgatgcc ccctggtttg tgtgttacgc acacacacgt 400
 gcacacaagg ctctggctcg cttccctccc tcgtttccag ctctggggcg 450
 aatcccacat ctgtttcaac tctccgccga gggcgagcag gagcgagagt 500
 gtgtcgaatc tgcgagtga gagggacgag ggaaaagaaa caaagccaca 550
 gacgcaactt gagactcccc catccccaaa gaagcaccag atcagcaaaa 600

aaagaagatg ggccccccga gcctcgtgct gtgcttgctg tccgcaactg 650
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 acaagacccg gcgcatcatg gagcagggcg gggcgcaatt catcaacgcc 850
 ttcgtgacca caccatgtg ctgccccca cgctcctcca tcctcactgg 900
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 cgccctcctg gcaggcacag cagcagagcc gcacctttgc cgtgtacctc 1000
 aatagcactg gctaccggac agctttcttc gggaagtatc ttaatgaata 1050
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 gatggaggaa gctatgagca atacaggcag tttcagcgtc gaaagtggcc 3150
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 ggggaaggta agaaacaaca gaggtggacc tccaaaaaca tagaggcatc 3250
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 aagaagcagg acagaggcaa cgtggagagg ctgaaaacag tgcagagacg 3700
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tttacatgta atcaacatgg gaacttttag gggaacctaa taagaaatcc 3850
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 gaaaaa 3906

<210> 84
 <211> 867
 <212> PRT
 <213> Homo sapiens

<400> 84
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 Leu Lys Gly Arg Phe Gln Arg Asp Arg Arg Asn Ile Arg Pro Asn
 35 40 45
 Ile Ile Leu Val Leu Thr Asp Asp Gln Asp Val Glu Leu Gly Ser
 50 55 60
 Met Gln Val Met Asn Lys Thr Arg Arg Ile Met Glu Gln Gly Gly
 65 70 75
 Ala His Phe Ile Asn Ala Phe Val Thr Thr Pro Met Cys Cys Pro
 80 85 90
 Ser Arg Ser Ser Ile Leu Thr Gly Lys Tyr Val His Asn His Asn
 95 100 105
 Thr Tyr Thr Asn Asn Glu Asn Cys Ser Ser Pro Ser Trp Gln Ala
 110 115 120
 Gln His Glu Ser Arg Thr Phe Ala Val Tyr Leu Asn Ser Thr Gly
 125 130 135
 Tyr Arg Thr Ala Phe Phe Gly Lys Tyr Leu Asn Glu Tyr Asn Gly
 140 145 150
 Ser Tyr Val Pro Pro Gly Trp Lys Glu Trp Val Gly Leu Leu Lys
 155 160 165
 Asn Ser Arg Phe Tyr Asn Tyr Thr Leu Cys Arg Asn Gly Val Lys
 170 175 180
 Glu Lys His Gly Ser Asp Tyr Ser Lys Asp Tyr Leu Thr Asp Leu
 185 190 195
 Ile Thr Asn Asp Ser Val Ser Phe Phe Arg Thr Ser Lys Lys Met
 200 205 210
 Tyr Pro His Arg Pro Val Leu Met Val Ile Ser His Ala Ala Pro
 215 220 225
 His Gly Pro Glu Asp Ser Ala Pro Gln Tyr Ser Arg Leu Phe Pro
 230 235 240
 Asn Ala Ser Gln His Ile Thr Pro Ser Tyr Asn Tyr Ala Pro Asn
 245 250 255

Pro	Asp	Lys	His	Trp	Ile	Met	Arg	Tyr	Thr	Gly	Pro	Met	Lys	Pro	
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Ile	His	Met	Glu	Phe	Thr	Asn	Met	Leu	Gln	Arg	Lys	Arg	Leu	Gln	
				275					280					285	
Thr	Leu	Met	Ser	Val	Asp	Asp	Ser	Met	Glu	Thr	Ile	Tyr	Asn	Met	
				290					295					300	
Leu	Val	Glu	Thr	Gly	Glu	Leu	Asp	Asn	Thr	Tyr	Ile	Val	Tyr	Thr	
				305					310					315	
Ala	Asp	His	Gly	Tyr	His	Ile	Gly	Gln	Phe	Gly	Leu	Val	Lys	Gly	
				320					325					330	
Lys	Ser	Met	Pro	Tyr	Glu	Phe	Asp	Ile	Arg	Val	Pro	Phe	Tyr	Val	
				335					340					345	
Arg	Gly	Pro	Asn	Val	Glu	Ala	Gly	Cys	Leu	Asn	Pro	His	Ile	Val	
				350					355					360	
Leu	Asn	Ile	Asp	Leu	Ala	Pro	Thr	Ile	Leu	Asp	Ile	Ala	Gly	Leu	
				365					370					375	
Asp	Ile	Pro	Ala	Asp	Met	Asp	Gly	Lys	Ser	Ile	Leu	Lys	Leu	Leu	
				380					385					390	
Asp	Thr	Glu	Arg	Pro	Val	Asn	Arg	Phe	His	Leu	Lys	Lys	Lys	Met	
				395					400					405	
Arg	Val	Trp	Arg	Asp	Ser	Phe	Leu	Val	Glu	Arg	Gly	Lys	Leu	Leu	
				410					415					420	
His	Lys	Arg	Asp	Asn	Asp	Lys	Val	Asp	Ala	Gln	Glu	Glu	Asn	Phe	
				425					430					435	
Leu	Pro	Lys	Tyr	Gln	Arg	Val	Lys	Asp	Leu	Cys	Gln	Arg	Ala	Glu	
				440					445					450	
Tyr	Gln	Thr	Ala	Cys	Glu	Gln	Leu	Gly	Gln	Lys	Trp	Gln	Cys	Val	
				455					460					465	
Glu	Asp	Ala	Thr	Gly	Lys	Leu	Lys	Leu	His	Lys	Cys	Lys	Gly	Pro	
				470					475					480	
Met	Arg	Leu	Gly	Gly	Ser	Arg	Ala	Leu	Ser	Asn	Leu	Val	Pro	Lys	
				485					490					495	
Tyr	Tyr	Gly	Gln	Gly	Ser	Glu	Ala	Cys	Thr	Cys	Asp	Ser	Gly	Asp	
				500					505					510	
Tyr	Lys	Leu	Ser	Leu	Ala	Gly	Arg	Arg	Lys	Lys	Leu	Phe	Lys	Lys	
				515					520					525	
Lys	Tyr	Lys	Ala	Ser	Tyr	Val	Arg	Ser	Arg	Ser	Ile	Arg	Ser	Val	
				530					535					540	
Ala	Ile	Glu	Val	Asp	Gly	Arg	Val	Tyr	His	Val	Gly	Leu	Gly	Asp	
				545					550					555	
Ala	Ala	Gln	Pro	Arg	Asn	Leu	Thr	Lys	Arg	His	Trp	Pro	Gly	Ala	
				560					565					570	

Pro	Glu	Asp	Gln	Asp	Asp	Lys	Asp	Gly	Gly	Asp	Phe	Ser	Gly	Thr	
				575					580					585	
Gly	Gly	Leu	Pro	Asp	Tyr	Ser	Ala	Ala	Asn	Pro	Ile	Lys	Val	Thr	
				590					595					600	
His	Arg	Cys	Tyr	Ile	Leu	Glu	Asn	Asp	Thr	Val	Gln	Cys	Asp	Leu	
				605					610					615	
Asp	Leu	Tyr	Lys	Ser	Leu	Gln	Ala	Trp	Lys	Asp	His	Lys	Leu	His	
				620					625					630	
Ile	Asp	His	Glu	Ile	Glu	Thr	Leu	Gln	Asn	Lys	Ile	Lys	Asn	Leu	
				635					640					645	
Arg	Glu	Val	Arg	Gly	His	Leu	Lys	Lys	Lys	Arg	Pro	Glu	Glu	Cys	
				650					655					660	
Asp	Cys	His	Lys	Ile	Ser	Tyr	His	Thr	Gln	His	Lys	Gly	Arg	Leu	
				665					670					675	
Lys	His	Arg	Gly	Ser	Ser	Leu	His	Pro	Phe	Arg	Lys	Gly	Leu	Gln	
				680					685					690	
Glu	Lys	Asp	Lys	Val	Trp	Leu	Leu	Arg	Glu	Gln	Lys	Arg	Lys	Lys	
				695					700					705	
Lys	Leu	Arg	Lys	Leu	Leu	Lys	Arg	Leu	Gln	Asn	Asn	Asp	Thr	Cys	
				710					715					720	
Ser	Met	Pro	Gly	Leu	Thr	Cys	Phe	Thr	His	Asp	Asn	Gln	His	Trp	
				725					730					735	
Gln	Thr	Ala	Pro	Phe	Trp	Thr	Leu	Gly	Pro	Phe	Cys	Ala	Cys	Thr	
				740					745					750	
Ser	Ala	Asn	Asn	Asn	Thr	Tyr	Trp	Cys	Met	Arg	Thr	Ile	Asn	Glu	
				755					760					765	
Thr	His	Asn	Phe	Leu	Phe	Cys	Glu	Phe	Ala	Thr	Gly	Phe	Leu	Glu	
				770					775					780	
Tyr	Phe	Asp	Leu	Asn	Thr	Asp	Pro	Tyr	Gln	Leu	Met	Asn	Ala	Val	
				785					790					795	
Asn	Thr	Leu	Asp	Arg	Asp	Val	Leu	Asn	Gln	Leu	His	Val	Gln	Leu	
				800					805					810	
Met	Glu	Leu	Arg	Ser	Cys	Lys	Gly	Tyr	Lys	Gln	Cys	Asn	Pro	Arg	
				815					820					825	
Thr	Arg	Asn	Met	Asp	Leu	Asp	Gly	Gly	Ser	Tyr	Glu	Gln	Tyr	Arg	
				830					835					840	
Gln	Phe	Gln	Arg	Arg	Lys	Trp	Pro	Glu	Met	Lys	Arg	Pro	Ser	Ser	
				845					850					855	
Lys	Ser	Leu	Gly	Gln	Leu	Trp	Glu	Gly	Trp	Glu	Gly				
				860					865						

<210> 85
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 <212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 85
gaagccggct gtctgaatc 19

<210> 86
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 86
ggccagctat ctccgcag 18

<210> 87
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 87
aagggcctgc aagagaag 18

<210> 88
<211> 18
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 88
cactgggaca actgtggg 18

<210> 89
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 89
cagaggcaac gtggagag 18

<210> 90
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 90
aagtattgtc atacagtgtt c 21

<210> 91
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 91
tagtacttgg gcacgaggtt ggag 24

<210> 92
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 92
tcataccaac tgctggtcat tggc 24

<210> 93
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 93
ctcaagctgc tggacacgga gcggccggtg aatcggtttc acttg 45

<210> 94
<211> 971
<212> DNA
<213> Homo sapiens

<400> 94
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aaggagtgag gagctgctgg gcagagaggg actgtccggc tcccagatgc 100
tgggcctcct ggggagcaca gccctcgtgg gatggatcac aggtgctgct 150
gtggcgggtcc tgctgctgct gctgctgctg gccacctgcc ttttccacgg 200
acggcaggac tgtgacgtgg agaggaaccg tacagctgca gggggaaacc 250
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atctttcacc atcaccgtca tcctggccac gtatctcatg tgccgaatgt 350
gggcctccac caccaccacc acccccgcca caccctcac cacctccacc 400
accaccacca cccccaccgc caccatcccc gccacgctcg ctgaggctgc 450
tgtgcgcggt gcctgtggac agcagctgcc cctgccctcc catctgttcc 500
caggacaagt ggaccccatg tttccatgtg gaaggatgca tctctggggt 550
gaacgagggg aacaatagac tggggcttgc tccagctgca tttgcatggc 600

cacgcttcac atacactaca cggaagctt ggtagatgga cgtattattg 300
acacctccct gaccagagac cctctgggta tagaacttgg ccaaaagcag 350
gtgattccag gtctggagca gagtcttctc gacatgtgtg tgggagagaa 400
gcgaagggca atcattccct ctcacttggc ctatggaaaa cggggatttc 450
caccatctgt cccagcggat gcagtgggtc agtatgacgt ggagctgatt 500
gcactaatcc gagccaacta ctggctaaag ctgggtgaagg gcattttgcc 550
tctggtaggg atggccatgg tgccagccct cctgggcctc attgggtatc 600
acctatacag aaaggccaat agacccaaag tctccaaaaa gaagctcaag 650
gaagagaaac gaaacaagag caaaaagaaa taataaataa taaattttaa 700
aaaacttaaa aaaaaaaaaa aaaaa 725

<210> 99
<211> 201
<212> PRT
<213> Homo sapiens

<400> 99
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1 5 10 15
Leu Leu Leu Ser Ala Ala Val Cys Arg Ala Glu Ala Gly Leu Glu
20 25 30
Thr Glu Ser Pro Val Arg Thr Leu Gln Val Glu Thr Leu Val Glu
35 40 45
Pro Pro Glu Pro Cys Ala Glu Pro Ala Ala Phe Gly Asp Thr Leu
50 55 60
His Ile His Tyr Thr Gly Ser Leu Val Asp Gly Arg Ile Ile Asp
65 70 75
Thr Ser Leu Thr Arg Asp Pro Leu Val Ile Glu Leu Gly Gln Lys
80 85 90
Gln Val Ile Pro Gly Leu Glu Gln Ser Leu Leu Asp Met Cys Val
95 100 105
Gly Glu Lys Arg Arg Ala Ile Ile Pro Ser His Leu Ala Tyr Gly
110 115 120
Lys Arg Gly Phe Pro Pro Ser Val Pro Ala Asp Ala Val Val Gln
125 130 135
Tyr Asp Val Glu Leu Ile Ala Leu Ile Arg Ala Asn Tyr Trp Leu
140 145 150
Lys Leu Val Lys Gly Ile Leu Pro Leu Val Gly Met Ala Met Val
155 160 165
Pro Ala Leu Leu Gly Leu Ile Gly Tyr His Leu Tyr Arg Lys Ala
170 175 180
Asn Arg Pro Lys Val Ser Lys Lys Lys Leu Lys Glu Glu Lys Arg

185

190

195

Asn Lys Ser Lys Lys Lys
200

<210> 100
<211> 705
<212> DNA
<213> Homo sapiens

<400> 100
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ccggctccct gccccgcgcc cagtcacgac cctgcgcccc tcaactcctcc 100
cgctccatct gctgctgctg ctgctgctca gtgcggcggt gtgccgggct 150
gaggctgggc tcgaaaccga aagtcccgtc cggaccctcc aagtggagac 200
cctggtggag cccccagaac catgtgccga gcccgctgct tttggagaca 250
cgcttcacat aactacacg ggaagcttgg tagatggacg tattattgac 300
acctccctga ccagagaccc tctggttata gaacttggcc aaaagcaggt 350
gattccaggt ctggagcaga gtcttctcga catgtgtgtg ggagagaagc 400
gaagggcaat cattccttct cacttggcct atggaaaacg gggatttcca 450
ccatctgtcc cagcggatgc agtggtgcag tatgacgtgg agctgattgc 500
actaatccga gccaaactact ggctaaagct ggtgaagggc attttgcctc 550
tggtagggat ggccatggtg ccaccctcct gggcctcatt gggatatcacc 600
tatacagaaa ggccaataga cccaaagtct ccaaaaagaa gctcaaggaa 650
gagaaacgaa acaagagcaa aaagaaataa taaataataa attttaaaaa 700
actta 705

<210> 101
<211> 543
<212> DNA
<213> Homo sapiens

<400> 101
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gaaccatgtg ccgagcccgcc tgcttttggg gacacgcttc acatacacta 100
cacgggaagc ttggtagatg gacgtattat tgacacctcc ctgaccagag 150
acctctggt tatagaactt ggccaaaagc aggtgattcc aggtctggag 200
cagagtcttc tcgacatgtg tgtgggagag aagcgaaggg caatcattcc 250
ttctcacttg gcctatggaa aacggggatt tccaccatct gtcccagcgg 300
atgcagtggg gcagtatgac gtggagctga ttgcactaat ccgagccaac 350
tactggctaa agctggtgaa gggcattttg cctctggtag ggatggccat 400

tccacatcca ccactg 1316

<210> 103
<211> 157
<212> PRT
<213> Homo sapiens

<400> 103
Met Ser Gly Phe Leu Glu Gly Leu Arg Cys Ser Glu Cys Ile Asp
1 5 10 15
Trp Gly Glu Lys Arg Asn Thr Ile Ala Ser Ile Ala Ala Gly Val
20 25 30
Leu Phe Phe Thr Gly Trp Trp Ile Ile Ile Asp Ala Ala Val Ile
35 40 45
Tyr Pro Thr Met Lys Asp Phe Asn His Ser Tyr His Ala Cys Gly
50 55 60
Val Ile Ala Thr Ile Ala Phe Leu Met Ile Asn Ala Val Ser Asn
65 70 75
Gly Gln Val Arg Gly Asp Ser Tyr Ser Glu Gly Cys Leu Gly Gln
80 85 90
Thr Gly Ala Arg Ile Trp Leu Phe Val Gly Phe Met Leu Ala Phe
95 100 105
Gly Ser Leu Ile Ala Ser Met Trp Ile Leu Phe Gly Gly Tyr Val
110 115 120
Ala Lys Glu Lys Asp Ile Val Tyr Pro Gly Ile Ala Val Phe Phe
125 130 135
Gln Asn Ala Phe Ile Phe Phe Gly Gly Leu Val Phe Lys Phe Gly
140 145 150
Arg Thr Glu Asp Leu Trp Gln
155

<210> 104
<211> 545
<212> DNA
<213> Homo sapiens

<400> 104
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ggctccggaa ccactgcacg acggggctgg actgacctga aaaaaatgtc 100
tggatttcta gagggcttga gatgctcaga atgcattgac tggggggaaa 150
agcgcaatac tattgcttcc attgctgctg gtgtactatt ttttacaggc 200
tggtggatta tcatagatgc agctgttatt tatcccacca tgaaagattt 250
caaccactca taccatgcct gtggtgttat agcaaccata gccttcctaa 300
tgattaatgc agtatcgaat ggacaagtcc gaggtgatag ttacagtga 350
ggttgtctgg gtcaaacagg tgctcgcatt tggtttttcg ttggtttcat 400

gttggccttt ggatctctga ttgcatctat gtggattctt tttggagggtt 450
 atgttgctaa agaaaaagac atagtatacc ctggaattgc tgtatttttc 500
 cagaatgcct tcatcttttt tggagggctg gtttttaagt ttggc 545

<210> 105
 <211> 490
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 31, 39, 108, 145, 179, 219, 412, 479
 <223> unknown base

<400> 105
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 agaatgcatg actgggggaa aagcgcaaat actattgctt ccattgctgc 100
 tgggtgtanta ttttttacag gctggtggat tatcatagat gcagntgtta 150
 tttatccac catgaaagat ttcaaccant cataccatgc ctgtggtgtt 200
 atagcaacca tagccttcnt aatgattaat gcagtatcga atggacaagt 250
 ccgaggtgat agttacagt aaggttggtt ggggtcaaaca ggtgctcgca 300
 tttggctttt cgttggtttc atgttggcct ttggatctct gattgcatct 350
 atgtggattc tttttggagg ttatgttgct aaagaaaaag acatagtata 400
 ccctggaatt gntgtatttt tccagaatgc cttcatcttt tttggagggc 450
 tggtttttaa gtttggccgc actgaagant tatggcagt 490

<210> 106
 <211> 466
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 26, 38, 81, 115, 207, 329, 380, 446, 449
 <223> unknown base

<400> 106
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 aatgttttga ttttttagagg gcttgagatg ntcagaatgc attgactggg 100
 ggaaaagcgc aatantattg ctttccattg ctgctggtgt actatttttt 150
 acaggggtggg ggattatcat agatgcagct gttatttata ccaccatgaa 200
 agattttnaac cactcatacc atgcctgtgg tgttatagca accatagcct 250
 tcctaataatg taatgcagta tcgaatggac aagtcgagg tgatagttac 300
 agtgaagggtt gtttgggtca aacaggtgnt cgcatttggc ttttcgttgg 350
 tttcatgttg gcctttggat ttctgattgn attctatgcg gattcttctt 400

ggagggttatg ttgctaaaga aaaagacata gtataccctg gaattnctnt 450

atccccccag aatgcc 466

<210> 107

<211> 377

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 52, 67, 70, 78, 105, 144, 150, 209, 266, 268, 282, 310, 331, 356

<223> unknown base

<400> 107

tagagggtctt gagatgctca gaatgcattg actgggggga aaagcgcaat 50

antattgctt ccattgntgn tgggtgnta tttttttaca ggctggtgga 100

ttatnataga tgcagctgtt atttatccca ccatgaaaga ttnaaccan 150

tcataccatg cctgtggtgt tatagcaacc atagccttcc taatgattaa 200

tgcagtatng aatggacaag tccgaggtga tagttacagt gaaggttggt 250

tgggtcaaac aggtgntngc atttggcttt tngttggttt catgttggcc 300

tttgatctn tgattgcatt tatgtggatt ntttttgag gttatgttgc 350

taaagnaaaa gacatagtat accctgt 377

<210> 108

<211> 552

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 12, 25, 65, 130, 437, 537

<223> unknown base

<400> 108

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ggccccggcgc ggcngacac cgggttccgg gaaccattgc acgacggggt 100

ggactgacct gaaaaaatg tttggatttn tagagggtt gagatgctca 150

gaatgcattg actgggggga aaagcgcaat actattgctt ccattgctgc 200

tgggtgtacta ttttttacag gctggtggat tatcatagat gcagctgtta 250

tttatccac catgaaagat ttcaaccact cataccatgc ctgtggtgtt 300

atagcaacca tagccttcct aatgattaat gcagtatcga atggacaagt 350

ccgaggtgat agttacagt aaggttgtct ggggtcaaaca ggtgctcgca 400

tttggttttt cggttggttc atgttggcct ttggatntct gattgcatct 450

atgtggattc tttttggagg ttatgttgct aaagaaaaag acatagtata 500

ccctggaatt gctgtatttt tccagaatgc cttcatnttt tttggagggc 550

tg 552

<210> 109
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 109
gggtggatgg tactgctgca tcc 23

<210> 110
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 110
tgttgtgctg tgggaaatca gatgtg 26

<210> 111
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 111
gtgtctggag gctgtggccg ttttgttttc ttgggctaaa atcggg 46

<210> 112
<211> 3004
<212> DNA
<213> Homo sapiens

<400> 112
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ccgaatcctt tctccgaaga tgtcaaacgg cccccagcgc ccctggtaac 150
tgacaaggag gccaggaaga aggttctcaa acaagctttt tcagccaacc 200
aagtgccgga gaagctggat gtggtggtaa ttggcagtgg ctttgggggc 250
ctggctgcag ctgcaattct agctaaagct ggcaagcgag tcctgggtgct 300
ggaacaacat accaaggcag ggggctgctg tcataccttt ggaaagaatg 350
gccttgaatt tgacacagga atccattaca ttgggcgtat ggaagagggc 400
agcattggcc gttttatctt ggaccagatc actgaagggc agctggactg 450
ggctcccctg tcctctcctt ttgacatcat ggtactggaa gggcccaatg 500
gccgaaagga gtaccccatg tacagtggag agaaagccta cattcagggc 550

ctcaaggaga agtttccaca ggaggaagct atcattgaca agtatataaa 600
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 tcctcccatt gcccggtggtt cagctcctcg acaggtgtgg gctgctgact 700
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 gcagcagctg ggggcctcct ctgagctcca ggagtgactc agctacatct 800
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 cagttatgtc tttggtatca gacatacgaa aggtctcttt gtagttcgtg 2950
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 aaaa 3004

<210> 113
 <211> 610
 <212> PRT
 <213> Homo sapiens

<400> 113
 Met Trp Leu Pro Leu Val Leu Leu Leu Ala Val Leu Leu Leu Ala
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 20 25 30
 Asn Pro Phe Ser Glu Asp Val Lys Arg Pro Pro Ala Pro Leu Val
 35 40 45
 Thr Asp Lys Glu Ala Arg Lys Lys Val Leu Lys Gln Ala Phe Ser
 50 55 60
 Ala Asn Gln Val Pro Glu Lys Leu Asp Val Val Val Ile Gly Ser
 65 70 75
 Gly Phe Gly Gly Leu Ala Ala Ala Ala Ile Leu Ala Lys Ala Gly
 80 85 90
 Lys Arg Val Leu Val Leu Glu Gln His Thr Lys Ala Gly Gly Cys
 95 100 105

Glu	Arg	Tyr	Val	Ser	Met	Pro	Arg	Glu	Glu	Ala	Ala	Glu	His	Ile	
				425					430					435	
Pro	Leu	Leu	Phe	Phe	Ala	Phe	Pro	Ser	Ala	Lys	Asp	Pro	Thr	Trp	
				440					445					450	
Glu	Asp	Arg	Phe	Pro	Gly	Arg	Ser	Thr	Met	Ile	Met	Leu	Ile	Pro	
				455					460					465	
Thr	Ala	Tyr	Glu	Trp	Phe	Glu	Glu	Trp	Gln	Ala	Glu	Leu	Lys	Gly	
				470					475					480	
Lys	Arg	Gly	Ser	Asp	Tyr	Glu	Thr	Phe	Lys	Asn	Ser	Phe	Val	Glu	
				485					490					495	
Ala	Ser	Met	Ser	Val	Val	Leu	Lys	Leu	Phe	Pro	Gln	Leu	Glu	Gly	
				500					505					510	
Lys	Val	Glu	Ser	Val	Thr	Ala	Gly	Ser	Pro	Leu	Thr	Asn	Gln	Phe	
				515					520					525	
Tyr	Leu	Ala	Ala	Pro	Arg	Gly	Ala	Cys	Tyr	Gly	Ala	Asp	His	Asp	
				530					535					540	
Leu	Gly	Arg	Leu	His	Pro	Cys	Val	Met	Ala	Ser	Leu	Arg	Ala	Gln	
				545					550					555	
Ser	Pro	Ile	Pro	Asn	Leu	Tyr	Leu	Thr	Gly	Gln	Asp	Ile	Phe	Thr	
				560					565					570	
Cys	Gly	Leu	Val	Gly	Ala	Leu	Gln	Gly	Ala	Leu	Leu	Cys	Ser	Ser	
				575					580					585	
Ala	Ile	Leu	Lys	Arg	Asn	Leu	Tyr	Ser	Asp	Leu	Lys	Asn	Leu	Asp	
				590					595					600	
Ser	Arg	Ile	Arg	Ala	Gln	Lys	Lys	Lys	Asn						
				605					610						

<210> 114
 <211> 1701
 <212> DNA
 <213> Homo sapiens

<400> 114
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 gatagggctg acgctgctgc tgtgtgcggt gctgctgagc ttggcctcgg 150
 cgtcctcgga tgaagaaggc agccaggatg aatccttaga ttccaagact 200
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 agttgctggt caaatatttc ttgattcaga agaattctgaa ttagaatcct 300
 ctattcaaga agaggaagac agcctcaaga gccaagaggg ggaaagtgtc 350
 acagaagata tcagctttct agagtctcca aatccagaaa acaaggacta 400
 tgaagagcca aagaaagtac ggaaaccagc ttgaccgcc attgaaggca 450

cagcacatgg ggagccctgc cacttccctt ttcttttcct agataaggag 500
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 tacaacctat gactacaaag cagatgaaaa gtggggcctt tgtgaaactg 600
 aagaagaggc tgctaagaga cggcagatgc aggaagcaga aatgatgtat 650
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 agaagcatat cggatatctc aaaaggcagc aagcatgaac cataccaaag 750
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 aatatccagg cagcgagaga gatgtttgag aagctgactg aggaaggctc 850
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 ttaattcaag tcaggcaaag gctcttgtat attatacatt tggagctctt 950
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<210> 115

<211> 301

<212> PRT

<213> Homo sapiens

<400> 115

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Leu Ser Leu Ala Ser Ala Ser Ser Asp Glu Glu Gly Ser Gln Asp
 20 25 30

Glu	Ser	Leu	Asp	Ser	Lys	Thr	Thr	Leu	Thr	Ser	Asp	Glu	Ser	Val
				35					40					45
Lys	Asp	His	Thr	Thr	Ala	Gly	Arg	Val	Val	Ala	Gly	Gln	Ile	Phe
				50					55					60
Leu	Asp	Ser	Glu	Glu	Ser	Glu	Leu	Glu	Ser	Ser	Ile	Gln	Glu	Glu
				65					70					75
Glu	Asp	Ser	Leu	Lys	Ser	Gln	Glu	Gly	Glu	Ser	Val	Thr	Glu	Asp
				80					85					90
Ile	Ser	Phe	Leu	Glu	Ser	Pro	Asn	Pro	Glu	Asn	Lys	Asp	Tyr	Glu
				95					100					105
Glu	Pro	Lys	Lys	Val	Arg	Lys	Pro	Ala	Leu	Thr	Ala	Ile	Glu	Gly
				110					115					120
Thr	Ala	His	Gly	Glu	Pro	Cys	His	Phe	Pro	Phe	Leu	Phe	Leu	Asp
				125					130					135
Lys	Glu	Tyr	Asp	Glu	Cys	Thr	Ser	Asp	Gly	Arg	Glu	Asp	Gly	Arg
				140					145					150
Leu	Trp	Cys	Ala	Thr	Thr	Tyr	Asp	Tyr	Lys	Ala	Asp	Glu	Lys	Trp
				155					160					165
Gly	Phe	Cys	Glu	Thr	Glu	Glu	Glu	Ala	Ala	Lys	Arg	Arg	Gln	Met
				170					175					180
Gln	Glu	Ala	Glu	Met	Met	Tyr	Gln	Thr	Gly	Met	Lys	Ile	Leu	Asn
				185					190					195
Gly	Ser	Asn	Lys	Lys	Ser	Gln	Lys	Arg	Glu	Ala	Tyr	Arg	Tyr	Leu
				200					205					210
Gln	Lys	Ala	Ala	Ser	Met	Asn	His	Thr	Lys	Ala	Leu	Glu	Arg	Val
				215					220					225
Ser	Tyr	Ala	Leu	Leu	Phe	Gly	Asp	Tyr	Leu	Pro	Gln	Asn	Ile	Gln
				230					235					240
Ala	Ala	Arg	Glu	Met	Phe	Glu	Lys	Leu	Thr	Glu	Glu	Gly	Ser	Pro
				245					250					255
Lys	Gly	Gln	Thr	Ala	Leu	Gly	Phe	Leu	Tyr	Ala	Ser	Gly	Leu	Gly
				260					265					270
Val	Asn	Ser	Ser	Gln	Ala	Lys	Ala	Leu	Val	Tyr	Tyr	Thr	Phe	Gly
				275					280					285
Ala	Leu	Gly	Gly	Asn	Leu	Ile	Ala	His	Met	Val	Leu	Val	Ser	Arg
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Leu

<210> 116

<211> 584

<212> DNA

<213> Homo sapiens

<400> 116

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<210> 117

<211> 123

<212> PRT

<213> Homo sapiens

<400> 117

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Ser	Val	Ser	Gln	Thr	Val	Leu	Ala	Gln	Leu	Asp	Ala	Leu	Leu	Val
			20						25					30
Phe	Pro	Gly	Gln	Val	Ala	Gln	Leu	Ser	Cys	Thr	Leu	Ser	Pro	Gln
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His	Val	Thr	Ile	Arg	Asp	Tyr	Gly	Val	Ser	Trp	Tyr	Gln	Gln	Arg
			50						55					60
Ala	Gly	Ser	Ala	Pro	Arg	Tyr	Leu	Leu	Tyr	Tyr	Arg	Ser	Glu	Glu
			65						70					75
Asp	His	His	Arg	Pro	Ala	Asp	Ile	Pro	Asp	Arg	Phe	Ser	Ala	Ala
			80						85					90
Lys	Asp	Glu	Ala	His	Asn	Ala	Cys	Val	Leu	Thr	Ile	Ser	Pro	Val
			95						100					105
Gln	Pro	Glu	Asp	Asp	Ala	Asp	Tyr	Tyr	Cys	Ser	Val	Gly	Tyr	Gly
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Phe Ser Pro

<210> 118

<211> 3402

<212> DNA

<213> Homo sapiens

<400> 118

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 aa 3402

<210> 119
 <211> 504
 <212> PRT
 <213> Homo sapiens

<400> 119
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 35 40 45
 Thr Val Arg Leu Gln Cys Pro Val Glu Gly Asp Pro Pro Pro Leu
 50 55 60
 Thr Met Trp Thr Lys Asp Gly Arg Thr Ile His Ser Gly Trp Ser
 65 70 75
 Arg Phe Arg Val Leu Pro Gln Gly Leu Lys Val Lys Gln Val Glu
 80 85 90
 Arg Glu Asp Ala Gly Val Tyr Val Cys Lys Ala Thr Asn Gly Phe
 95 100 105
 Gly Ser Leu Ser Val Asn Tyr Thr Leu Val Val Leu Asp Asp Ile
 110 115 120
 Ser Pro Gly Lys Glu Ser Leu Gly Pro Asp Ser Ser Ser Gly Gly
 125 130 135
 Gln Glu Asp Pro Ala Ser Gln Gln Trp Ala Arg Pro Arg Phe Thr
 140 145 150
 Gln Pro Ser Lys Met Arg Arg Arg Val Ile Ala Arg Pro Val Gly
 155 160 165
 Ser Ser Val Arg Leu Lys Cys Val Ala Ser Gly His Pro Arg Pro
 170 175 180
 Asp Ile Thr Trp Met Lys Asp Asp Gln Ala Leu Thr Arg Pro Glu
 185 190 195
 Ala Ala Glu Pro Arg Lys Lys Lys Trp Thr Leu Ser Leu Lys Asn
 200 205 210
 Leu Arg Pro Glu Asp Ser Gly Lys Tyr Thr Cys Arg Val Ser Asn
 215 220 225
 Arg Ala Gly Ala Ile Asn Ala Thr Tyr Lys Val Asp Val Ile Gln
 230 235 240

Arg	Thr	Arg	Ser	Lys	Pro	Val	Leu	Thr	Gly	Thr	His	Pro	Val	Asn
				245					250					255
Thr	Thr	Val	Asp	Phe	Gly	Gly	Thr	Thr	Ser	Phe	Gln	Cys	Lys	Val
				260					265					270
Arg	Ser	Asp	Val	Lys	Pro	Val	Ile	Gln	Trp	Leu	Lys	Arg	Val	Glu
				275					280					285
Tyr	Gly	Ala	Glu	Gly	Arg	His	Asn	Ser	Thr	Ile	Asp	Val	Gly	Gly
				290					295					300
Gln	Lys	Phe	Val	Val	Leu	Pro	Thr	Gly	Asp	Val	Trp	Ser	Arg	Pro
				305					310					315
Asp	Gly	Ser	Tyr	Leu	Asn	Lys	Leu	Leu	Ile	Thr	Arg	Ala	Arg	Gln
				320					325					330
Asp	Asp	Ala	Gly	Met	Tyr	Ile	Cys	Leu	Gly	Ala	Asn	Thr	Met	Gly
				335					340					345
Tyr	Ser	Phe	Arg	Ser	Ala	Phe	Leu	Thr	Val	Leu	Pro	Asp	Pro	Lys
				350					355					360
Pro	Pro	Gly	Pro	Pro	Val	Ala	Ser	Ser	Ser	Ser	Ala	Thr	Ser	Leu
				365					370					375
Pro	Trp	Pro	Val	Val	Ile	Gly	Ile	Pro	Ala	Gly	Ala	Val	Phe	Ile
				380					385					390
Leu	Gly	Thr	Leu	Leu	Leu	Trp	Leu	Cys	Gln	Ala	Gln	Lys	Lys	Pro
				395					400					405
Cys	Thr	Pro	Ala	Pro	Ala	Pro	Pro	Leu	Pro	Gly	His	Arg	Pro	Pro
				410					415					420
Gly	Thr	Ala	Arg	Asp	Arg	Ser	Gly	Asp	Lys	Asp	Leu	Pro	Ser	Leu
				425					430					435
Ala	Ala	Leu	Ser	Ala	Gly	Pro	Gly	Val	Gly	Leu	Cys	Glu	Glu	His
				440					445					450
Gly	Ser	Pro	Ala	Ala	Pro	Gln	His	Leu	Leu	Gly	Pro	Gly	Pro	Val
				455					460					465
Ala	Gly	Pro	Lys	Leu	Tyr	Pro	Lys	Leu	Tyr	Thr	Asp	Ile	His	Thr
				470					475					480
His	Thr	His	Thr	His	Ser	His	Thr	His	Ser	His	Val	Glu	Gly	Lys
				485					490					495
Val	His	Gln	His	Ile	His	Tyr	Gln	Cys						
				500										

<210> 120

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 120

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<210> 121

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 121

cggttcgaca cgcggcaggt g 21

<210> 122

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 122

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<210> 123

<211> 4420

<212> DNA

<213> Homo sapiens

<400> 123

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 catggttttg cccacctctg caatagtgat aatctgatgc tgaagatcaa 4050

Gln	Val	Asn	Ala	Asp	Cys	Asp	Ala	Cys	Met	Cys	Gln	Asp	Phe	Met	215	220	225
Leu	His	Gly	Ala	Val	Ser	Leu	Pro	Gly	Gly	Ala	Pro	Ala	Ser	Gly	230	235	240
Ala	Ala	Ile	Tyr	Leu	Leu	Thr	Lys	Thr	Pro	Lys	Leu	Leu	Thr	Gln	245	250	255
Thr	Asp	Ser	Asp	Gly	Arg	Phe	Arg	Ile	Pro	Gly	Leu	Cys	Pro	Asp	260	265	270
Gly	Lys	Ser	Ile	Leu	Lys	Ile	Thr	Lys	Val	Lys	Phe	Ala	Pro	Ile	275	280	285
Val	Leu	Thr	Met	Pro	Lys	Thr	Ser	Leu	Lys	Ala	Ala	Thr	Ile	Lys	290	295	300
Ala	Glu	Phe	Val	Arg	Ala	Glu	Thr	Pro	Tyr	Met	Val	Met	Asn	Pro	305	310	315
Glu	Thr	Lys	Ala	Arg	Arg	Ala	Gly	Gln	Ser	Val	Ser	Leu	Cys	Cys	320	325	330
Lys	Ala	Thr	Gly	Lys	Pro	Arg	Pro	Asp	Lys	Tyr	Phe	Trp	Tyr	His	335	340	345
Asn	Asp	Thr	Leu	Leu	Asp	Pro	Ser	Leu	Tyr	Lys	His	Glu	Ser	Lys	350	355	360
Leu	Val	Leu	Arg	Lys	Leu	Gln	Gln	His	Gln	Ala	Gly	Glu	Tyr	Phe	365	370	375
Cys	Lys	Ala	Gln	Ser	Asp	Ala	Gly	Ala	Val	Lys	Ser	Lys	Val	Ala	380	385	390
Gln	Leu	Ile	Val	Thr	Ala	Ser	Asp	Glu	Thr	Pro	Cys	Asn	Pro	Val	395	400	405
Pro	Glu	Ser	Tyr	Leu	Ile	Arg	Leu	Pro	His	Asp	Cys	Phe	Gln	Asn	410	415	420
Ala	Thr	Asn	Ser	Phe	Tyr	Tyr	Asp	Val	Gly	Arg	Cys	Pro	Val	Lys	425	430	435
Thr	Cys	Ala	Gly	Gln	Gln	Asp	Asn	Gly	Ile	Arg	Cys	Arg	Asp	Ala	440	445	450
Val	Gln	Asn	Cys	Cys	Gly	Ile	Ser	Lys	Thr	Glu	Glu	Arg	Glu	Ile	455	460	465
Gln	Cys	Ser	Gly	Tyr	Thr	Leu	Pro	Thr	Lys	Val	Ala	Lys	Glu	Cys	470	475	480
Ser	Cys	Gln	Arg	Cys	Thr	Glu	Thr	Arg	Ser	Ile	Val	Arg	Gly	Arg	485	490	495
Val	Ser	Ala	Ala	Asp	Asn	Gly	Glu	Pro	Met	Arg	Phe	Gly	His	Val	500	505	510
Tyr	Met	Gly	Asn	Ser	Arg	Val	Ser	Met	Thr	Gly	Tyr	Lys	Gly	Thr	515	520	525

Phe Thr Leu His Val Pro Gln Asp Thr Glu Arg Leu Val Leu Thr	530	535	540
Phe Val Asp Arg Leu Gln Lys Phe Val Asn Thr Thr Lys Val Leu	545	550	555
Pro Phe Asn Lys Lys Gly Ser Ala Val Phe His Glu Ile Lys Met	560	565	570
Leu Arg Arg Lys Glu Pro Ile Thr Leu Glu Ala Met Glu Thr Asn	575	580	585
Ile Ile Pro Leu Gly Glu Val Val Gly Glu Asp Pro Met Ala Glu	590	595	600
Leu Glu Ile Pro Ser Arg Ser Phe Tyr Arg Gln Asn Gly Glu Pro	605	610	615
Tyr Ile Gly Lys Val Lys Ala Ser Val Thr Phe Leu Asp Pro Arg	620	625	630
Asn Ile Ser Thr Ala Thr Ala Ala Gln Thr Asp Leu Asn Phe Ile	635	640	645
Asn Asp Glu Gly Asp Thr Phe Pro Leu Arg Thr Tyr Gly Met Phe	650	655	660
Ser Val Asp Phe Arg Asp Glu Val Thr Ser Glu Pro Leu Asn Ala	665	670	675
Gly Lys Val Lys Val His Leu Asp Ser Thr Gln Val Lys Met Pro	680	685	690
Glu His Ile Ser Thr Val Lys Leu Trp Ser Leu Asn Pro Asp Thr	695	700	705
Gly Leu Trp Glu Glu Glu Gly Asp Phe Lys Phe Glu Asn Gln Arg	710	715	720
Arg Asn Lys Arg Glu Asp Arg Thr Phe Leu Val Gly Asn Leu Glu	725	730	735
Ile Arg Glu Arg Arg Leu Phe Asn Leu Asp Val Pro Glu Ser Arg	740	745	750
Arg Cys Phe Val Lys Val Arg Ala Tyr Arg Ser Glu Arg Phe Leu	755	760	765
Pro Ser Glu Gln Ile Gln Gly Val Val Ile Ser Val Ile Asn Leu	770	775	780
Glu Pro Arg Thr Gly Phe Leu Ser Asn Pro Arg Ala Trp Gly Arg	785	790	795
Phe Asp Ser Val Ile Thr Gly Pro Asn Gly Ala Cys Val Pro Ala	800	805	810
Phe Cys Asp Asp Gln Ser Pro Asp Ala Tyr Ser Ala Tyr Val Leu	815	820	825
Ala Ser Leu Ala Gly Glu Glu Leu Gln Ala Val Glu Ser Ser Pro	830	835	840

Lys	Phe	Asn	Pro	Asn	Ala	Ile	Gly	Val	Pro	Gln	Pro	Tyr	Leu	Asn	
				845					850					855	
Lys	Leu	Asn	Tyr	Arg	Arg	Thr	Asp	His	Glu	Asp	Pro	Arg	Val	Lys	
				860					865					870	
Lys	Thr	Ala	Phe	Gln	Ile	Ser	Met	Ala	Lys	Pro	Arg	Pro	Asn	Ser	
				875					880					885	
Ala	Glu	Glu	Ser	Asn	Gly	Pro	Ile	Tyr	Ala	Phe	Glu	Asn	Leu	Arg	
				890					895					900	
Ala	Cys	Glu	Glu	Ala	Pro	Pro	Ser	Ala	Ala	His	Phe	Arg	Phe	Tyr	
				905					910					915	
Gln	Ile	Glu	Gly	Asp	Arg	Tyr	Asp	Tyr	Asn	Thr	Val	Pro	Phe	Asn	
				920					925					930	
Glu	Asp	Asp	Pro	Met	Ser	Trp	Thr	Glu	Asp	Tyr	Leu	Ala	Trp	Trp	
				935					940					945	
Pro	Lys	Pro	Met	Glu	Phe	Arg	Ala	Cys	Tyr	Ile	Lys	Val	Lys	Ile	
				950					955					960	
Val	Gly	Pro	Leu	Glu	Val	Asn	Val	Arg	Ser	Arg	Asn	Met	Gly	Gly	
				965					970					975	
Thr	His	Arg	Arg	Thr	Val	Gly	Lys	Leu	Tyr	Gly	Ile	Arg	Asp	Val	
				980					985					990	
Arg	Ser	Thr	Arg	Asp	Arg	Asp	Gln	Pro	Asn	Val	Ser	Ala	Ala	Cys	
				995					1000					1005	
Leu	Glu	Phe	Lys	Cys	Ser	Gly	Met	Leu	Tyr	Asp	Gln	Asp	Arg	Val	
				1010					1015					1020	
Asp	Arg	Thr	Leu	Val	Lys	Val	Ile	Pro	Gln	Gly	Ser	Cys	Arg	Arg	
				1025					1030					1035	
Ala	Ser	Val	Asn	Pro	Met	Leu	His	Glu	Tyr	Leu	Val	Asn	His	Leu	
				1040					1045					1050	
Pro	Leu	Ala	Val	Asn	Asn	Asp	Thr	Ser	Glu	Tyr	Thr	Met	Leu	Ala	
				1055					1060					1065	
Pro	Leu	Asp	Pro	Leu	Gly	His	Asn	Tyr	Gly	Ile	Tyr	Thr	Val	Thr	
				1070					1075					1080	
Asp	Gln	Asp	Pro	Arg	Thr	Ala	Lys	Glu	Ile	Ala	Leu	Gly	Arg	Cys	
				1085					1090					1095	
Phe	Asp	Gly	Thr	Ser	Asp	Gly	Ser	Ser	Arg	Ile	Met	Lys	Ser	Asn	
				1100					1105					1110	
Val	Gly	Val	Ala	Leu	Thr	Phe	Asn	Cys	Val	Glu	Arg	Gln	Val	Gly	
				1115					1120					1125	
Arg	Gln	Ser	Ala	Phe	Gln	Tyr	Leu	Gln	Ser	Thr	Pro	Ala	Gln	Ser	
				1130					1135					1140	
Pro	Ala	Ala	Gly	Thr	Val	Gln	Gly	Arg	Val	Pro	Ser	Arg	Arg	Gln	
				1145					1150					1155	

Gln Arg Ala Ser Arg Gly Gly Gln Arg Gln Gly Gly Val Val Ala
 1160 1165 1170
 Ser Leu Arg Phe Pro Arg Val Ala Gln Gln Pro Leu Ile Asn
 1175 1180

<210> 125
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 125
 ctggtgcctc aacagggagc ag 22

<210> 126
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 126
 ccattgtgca ggtcaggtca cag 23

<210> 127
 <211> 40
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 127
 ctggagcaag tgctcagctg cctgtggtca gactggggtc 40

<210> 128
 <211> 2819
 <212> DNA
 <213> Homo sapiens

<400> 128
 ctgcaagttg ttaacgccta acacacaagt atgttaggct tccaccaaag 50
 tcttcaatat acctgaatac gcacaatatc ttaactcttc atatttggtt 100
 ttgggatctg ctttgaggtc ccatcttcat ttaaaaaaaaa atacagagac 150
 ctacctaccc gtacgcatac atacatatgt gtatatatat gtaaaactaga 200
 caaagatcgc agatcataaa gcaagctctg ctttagtttc caagaagatt 250
 acaaagaatt tagagatgta tttgtcaaga tccctgtcga ttcatgccct 300
 ttgggttacg gtgtcctcag tgatgcagcc ctaccctttg gtttggggac 350
 attatgattt gtgtaagact cagatttaca cggaagaagg gaaagtttgg 400
 gattacatgg cctgccagcc ggaatccacg gacatgacaa aatatctgaa 450

agtgaaactc gatcctccgg atattacctg tggagaccct cctgagacgt 500
 tctgtgcaat gggcaatccc tacatgtgca ataatgagtg tgatgcgagt 550
 acccctgagc tggcacaccc ccctgagctg atgtttgatt ttgaaggaag 600
 acatccctcc acattttggc agtctgccac ttggaaggag tatcccaagc 650
 ctctccaggt taacatcact ctgtcttggg gcaaaacat tgagctaaca 700
 gacaacatag ttattacctt tgaatctggg cgtccagacc aaatgatcct 750
 ggagaagtct ctcgattatg gacgaacatg gcagccctat cagtattatg 800
 ccacagactg cttagatgct ttccacatgg atcctaaatc cgtgaaggat 850
 ttatcacagc atacggtctt agaaatcatt tgcacagaag agtactcaac 900
 aggggtataca acaaatagca aaataatcca ctttgaaatc aaagacagggt 950
 tcgcgccttt tgctggacct cgcctacgca atatggcttc cctctacgga 1000
 cagctggata caaccaagaa actcagagat ttcttttacag tcacagacct 1050
 gaggataagg ctgttaagac cagccgttgg ggaaatattt gtagatgagc 1100
 tacacttggc acgctacttt tacgcgatct cagacataaa ggtgcgagga 1150
 aggtgcaagt gtaatctcca tgccactgta tgtgtgtatg acaacagcaa 1200
 attgacatgc gaatgtgagc acaacactac aggtccagac tgtgggaaat 1250
 gcaagaagaa ttatcagggc cgaccttggg gtccaggctc ctatctcccc 1300
 atccccaaag gcaactgcaa tacctgtatc ccagtatatt ccagtattgg 1350
 tacgaatgtc tgcgacaacg agctcctgca ctgccagaac ggagggacgt 1400
 gccacaacaa cgtgcgctgc ctgtgcccgg ccgcatacac gggcatcctc 1450
 tgcgagaagc tgcggtgoga ggaggctggc agctgcggct ccgactctgg 1500
 ccagggcgcg ccccgacagc gcaccccagc gctgctgctg ctgaccacgc 1550
 tgctgggaac cgcagcccc ctggtgttct aggtgtcacc tccagccaca 1600
 ccggacgggc ctgtgccgtg gggaagcaga cacaacccaa acatttgcta 1650
 ctaacatagg aaacacacac atacagacac cccactcag acagtgtaca 1700
 aactaagaag gcctaactga actaagccat atttatcacc cgtggacagc 1750
 acatccgagt caagactgtt aatttctgac tccagaggag ttggcagctg 1800
 ttgatattat cactgcaa at cacattgcca gctgcagagc atattgtgga 1850
 ttggaaaggc tgcgacagcc ccccaaacag gaaagacaaa aaacaaacaa 1900
 atcaaccgac ctaaaaacat tggctactct agcgtggtgc gccctagtag 1950
 gactccgccc agtgtgtgga ccaaccaa at agcattcttt gctgtcaggt 2000
 gcattgtggg cataaggaaa tctgttacia gctgccatat tggcctgctt 2050

ccgtccctga atcccttcca acctgtgctt tagtgaacgt tgctctgtaa 2100
 ccctcggttg ttgaaagatt tctttgtctg atgttagtga tgcacatgtg 2150
 taacagcccc ctctaaaagc gcaagccagt catacccctg tatactcttag 2200
 cagcactgag tccagtgcga gcacacaccc actatacaag agtggctata 2250
 ggaaaaaaga aagtgtatct atccttttgt attcaaatga agttattttt 2300
 cttgaactac tgtaatatgt agattttttg tattattgcc aatttgtgtt 2350
 accagacaat ctgttaatat atctaattcg aatcagcaaa gactgacatt 2400
 ttattttgtc ctctttcgtt ctgttttgtt tcaactgtgca gagatttctc 2450
 tgtaagggca acgaacgtgc tggcatcaaa gaatatcagt ttacatatat 2500
 aacaagtgtg ataagattcc accaaaggac attctaaatg ttttcttgtt 2550
 gctttaacac tggaagattt aaagaataaa aactcctgca taaacgattt 2600
 caggaatttg tattgcaatt tcttaagatg aaaggaacag ccaccaagca 2650
 gtttcacact cactttactg atttctgtgt ggactgagta cattcagctg 2700
 acgaatttag ttcccaggaa gatggattga tgttcactag cttggacaac 2750
 ttctgcaaaa tatgagacta tttccacttg ggaaaaatta caacagcaaa 2800
 aaaaaaaaaa aaaaaaaaaa 2819

<210> 129
 <211> 438
 <212> PRT
 <213> Homo sapiens

<400> 129
 Met Tyr Leu Ser Arg Ser Leu Ser Ile His Ala Leu Trp Val Thr
 1 5 10 15
 Val Ser Ser Val Met Gln Pro Tyr Pro Leu Val Trp Gly His Tyr
 20 25 30
 Asp Leu Cys Lys Thr Gln Ile Tyr Thr Glu Glu Gly Lys Val Trp
 35 40 45
 Asp Tyr Met Ala Cys Gln Pro Glu Ser Thr Asp Met Thr Lys Tyr
 50 55 60
 Leu Lys Val Lys Leu Asp Pro Pro Asp Ile Thr Cys Gly Asp Pro
 65 70 75
 Pro Glu Thr Phe Cys Ala Met Gly Asn Pro Tyr Met Cys Asn Asn
 80 85 90
 Glu Cys Asp Ala Ser Thr Pro Glu Leu Ala His Pro Pro Glu Leu
 95 100 105
 Met Phe Asp Phe Glu Gly Arg His Pro Ser Thr Phe Trp Gln Ser
 110 115 120
 Ala Thr Trp Lys Glu Tyr Pro Lys Pro Leu Gln Val Asn Ile Thr

	125		130		135
Leu Ser Trp Ser	Lys Thr Ile Glu Leu	Thr Asp Asn Ile Val	Ile		
	140		145		150
Thr Phe Glu Ser	Gly Arg Pro Asp Gln	Met Ile Leu Glu Lys	Ser		
	155		160		165
Leu Asp Tyr Gly	Arg Thr Trp Gln Pro	Tyr Gln Tyr Tyr Ala	Thr		
	170		175		180
Asp Cys Leu Asp	Ala Phe His Met Asp	Pro Lys Ser Val Lys	Asp		
	185		190		195
Leu Ser Gln His	Thr Val Leu Glu Ile	Ile Cys Thr Glu Glu	Tyr		
	200		205		210
Ser Thr Gly Tyr	Thr Thr Asn Ser Lys	Ile Ile His Phe Glu	Ile		
	215		220		225
Lys Asp Arg Phe	Ala Leu Phe Ala Gly	Pro Arg Leu Arg Asn	Met		
	230		235		240
Ala Ser Leu Tyr	Gly Gln Leu Asp Thr	Thr Lys Lys Leu Arg	Asp		
	245		250		255
Phe Phe Thr Val	Thr Asp Leu Arg Ile	Arg Leu Leu Arg Pro	Ala		
	260		265		270
Val Gly Glu Ile	Phe Val Asp Glu Leu	His Leu Ala Arg Tyr	Phe		
	275		280		285
Tyr Ala Ile Ser	Asp Ile Lys Val Arg	Gly Arg Cys Lys Cys	Asn		
	290		295		300
Leu His Ala Thr	Val Cys Val Tyr Asp	Asn Ser Lys Leu Thr	Cys		
	305		310		315
Glu Cys Glu His	Asn Thr Thr Gly Pro	Asp Cys Gly Lys Cys	Lys		
	320		325		330
Lys Asn Tyr Gln	Gly Arg Pro Trp Ser	Pro Gly Ser Tyr Leu	Pro		
	335		340		345
Ile Pro Lys Gly	Thr Ala Asn Thr Cys	Ile Pro Ser Ile Ser	Ser		
	350		355		360
Ile Gly Thr Asn	Val Cys Asp Asn Glu	Leu Leu His Cys Gln	Asn		
	365		370		375
Gly Gly Thr Cys	His Asn Asn Val Arg	Cys Leu Cys Pro Ala	Ala		
	380		385		390
Tyr Thr Gly Ile	Leu Cys Glu Lys Leu	Arg Cys Glu Glu Ala	Gly		
	395		400		405
Ser Cys Gly Ser	Asp Ser Gly Gln Gly	Ala Pro Pro His Gly	Thr		
	410		415		420
Pro Ala Leu Leu	Leu Leu Thr Thr Leu	Leu Gly Thr Ala Ser	Pro		
	425		430		435
Leu Val Phe					

<210> 130
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 130
 tcgattatgg acgaacatgg cagc 24

<210> 131
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 131
 ttctgagatc cctcatcctc 20

<210> 132
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 132
 aggttcaggg acagcaagtt tggg 24

<210> 133
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 133
 ttgtctggac ctccggtacg gaattggctt ccctctacgg acagctggat 50

<210> 134
 <211> 1493
 <212> DNA
 <213> Homo sapiens

<400> 134
 cccacgcgtc cgggtgacct gggccgagcc ctcccggctg gctaagattg 50
 ctgaggaggc ggcgggtagc tggcaggcgc cgacttccga aggccgccgt 100
 ccgggcgagg tgtcctcatg acttctcttg tggaccatgt ccgtgatctt 150
 ttttgcctgc gtggtacggg taagggatgg actgcccctc tcagcctcta 200
 ctgattttta ccacacccaa gatttttttg aatggaggag acggctcaag 250
 agtttagcct tgcgactggc ccagtatcca ggtcgagggt ctgcagaagg 300

ttgtgacttt agtatacatt tttcttcttt cggggacgtg gcctgcatgg 350
 ctatctgctc ctgccagtgt ccagcagcca tggccttctg cttcctggag 400
 accctgtggg ggaattcac agcttcctat gacactacct gcattggcct 450
 agcctccagg ccatacgctt ttcttgagtt tgacagcatc attcagaaag 500
 tgaagtggca ttttaactat gtaagttcct ctcagatgga gtgcagcttg 550
 gaaaaaattc aggaggagct caagttgcag cctccagcgg ttctcactct 600
 ggaggacaca gatgtggcaa atgggggtgat gaatggtcac acaccgatgc 650
 acttgagacc tgctcctaatt tccgaatgg aaccagtgac agccctgggt 700
 atcctctccc tcattctcaa catcatgtgt gctgccctga atctcattcg 750
 aggagttcac cttgcagaac attctttaca ggatccaagg agctgggttct 800
 gctggttgga ccaaactcgt tgagccagcc acccctgacc caaatgagga 850
 gagctctgat tctcccatcc gggagcagtg atgtcaaact tctgctgctg 900
 gggaaatctc atcagcaggg agcctgtgga aaagggcatg tcagtgaat 950
 ctgggaatgg ctggattcgg aaacatctgc ccatgtgtat tgatggcaga 1000
 gctggtgccc acaagcgctt tttatttagg gtaaaattaa caaatccatt 1050
 ctattcctct gacctatgct tagtacatat gacctttaac cttacattt 1100
 atatgattct ggggttgctt cagaagtgtt atttcatgaa tcattcatat 1150
 gatttgatcc cccaggattc tattttgttt aatgggcttt tctactaaaa 1200
 gcataaaata ctgaggctga tttagtcagg gcaaaacat ttactttaca 1250
 tattcgTTTT caatacttgc tgttcatgtt acacaagctt cttacggttt 1300
 tcttgtaaca ataaatatTT tgagtaaata atgggtacat ttttaacaaac 1350
 tcagtagtac aacctaaact tgtataaaag tgtgtaaaaa tgtatagcca 1400
 tttatatcct atgtataaat taaatgaggt ggcttcagaa atggcagaat 1450
 aaatctaaag tgtttattaa aaaaaaaaaa aaaaaaaaaa aag 1493

<210> 135
 <211> 228
 <212> PRT
 <213> Homo sapiens

<400> 135
 Met Ser Val Ile Phe Phe Ala Cys Val Val Arg Val Arg Asp Gly
 1 5 10 15
 Leu Pro Leu Ser Ala Ser Thr Asp Phe Tyr His Thr Gln Asp Phe
 20 25 30
 Leu Glu Trp Arg Arg Arg Leu Lys Ser Leu Ala Leu Arg Leu Ala
 35 40 45

Gln	Tyr	Pro	Gly	Arg	Gly	Ser	Ala	Glu	Gly	Cys	Asp	Phe	Ser	Ile	
				50					55					60	
His	Phe	Ser	Ser	Phe	Gly	Asp	Val	Ala	Cys	Met	Ala	Ile	Cys	Ser	
				65					70					75	
Cys	Gln	Cys	Pro	Ala	Ala	Met	Ala	Phe	Cys	Phe	Leu	Glu	Thr	Leu	
				80					85					90	
Trp	Trp	Glu	Phe	Thr	Ala	Ser	Tyr	Asp	Thr	Thr	Cys	Ile	Gly	Leu	
				95					100					105	
Ala	Ser	Arg	Pro	Tyr	Ala	Phe	Leu	Glu	Phe	Asp	Ser	Ile	Ile	Gln	
				110					115					120	
Lys	Val	Lys	Trp	His	Phe	Asn	Tyr	Val	Ser	Ser	Ser	Gln	Met	Glu	
				125					130					135	
Cys	Ser	Leu	Glu	Lys	Ile	Gln	Glu	Glu	Leu	Lys	Leu	Gln	Pro	Pro	
				140					145					150	
Ala	Val	Leu	Thr	Leu	Glu	Asp	Thr	Asp	Val	Ala	Asn	Gly	Val	Met	
				155					160					165	
Asn	Gly	His	Thr	Pro	Met	His	Leu	Glu	Pro	Ala	Pro	Asn	Phe	Arg	
				170					175					180	
Met	Glu	Pro	Val	Thr	Ala	Leu	Gly	Ile	Leu	Ser	Leu	Ile	Leu	Asn	
				185					190					195	
Ile	Met	Cys	Ala	Ala	Leu	Asn	Leu	Ile	Arg	Gly	Val	His	Leu	Ala	
				200					205					210	
Glu	His	Ser	Leu	Gln	Asp	Pro	Arg	Ser	Trp	Phe	Cys	Trp	Leu	Asp	
				215					220					225	

Gln Thr Ser

<210> 136
 <211> 239
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 39, 61, 143, 209
 <223> unknown base

<400> 136
 tgcttcctgg agaccctgtg gtgggaattc acagcttcnt atgacactac 50
 ctgcattggc ntaccctcca ggccatacgc ttttcttgag ttgacagca 100
 tcattcagaa agtgaagtgg cattttaact atgtaagttc ctntcagatg 150
 gaggtcagct tggaaaaaat tcaggaggag ctcaagttgc agcctccagc 200
 gggttcant atggaggaca cagatgtggc aaatgggggt 239

<210> 137
 <211> 2300
 <212> DNA

<213> Homo sapiens

<400> 137

ctcagcggcg cttcctcgta gcgagcctag tggcgggtgt ttgcattgaa 50
acgtgagcgc gacccgacct taaagagtgg ggagcaaagg gaggacagag 100
ccctttaaaa cgaggcgggt ggtgcctgcc cctttaaggg cggggcgtcc 150
ggacgactgt atctgagccc cagactgccc cgagtttctg tcgcaggctg 200
cgaggaaagg cccctaggct gggctctgggt gcttggcggc ggcggcttcc 250
tccccgctcg tctccccgg gccagaggc acctcggtt cagtcatgct 300
gagcagagta tgggaagcacc tgactacgaa gtgctatccg tgcgagaaca 350
gctattccac gagaggatcc gcgagtgtat tatatcaaca cttctgtttg 400
caacactgta catcctctgc cacatcttcc tgaccgctt caagaagcct 450
gctgagttca ccacagtgga tgatgaagat gccaccgtca acaagattgc 500
gctcgagctg tgcaccttta ccctggcaat tgccctgggt gctgtcctgc 550
tcttgccctt ctccatcatc agcaatgagg tgctgctctc cctgcctcgg 600
aactactaca tccagtggct caacggctcc ctcatccatg gcctctggaa 650
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<210> 138
<211> 489
<212> PRT
<213> Homo sapiens

<400> 138
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20 25 30
Ala Thr Leu Tyr Ile Leu Cys His Ile Phe Leu Thr Arg Phe Lys
35 40 45
Lys Pro Ala Glu Phe Thr Thr Val Asp Asp Glu Asp Ala Thr Val
50 55 60
Asn Lys Ile Ala Leu Glu Leu Cys Thr Phe Thr Leu Ala Ile Ala
65 70 75
Leu Gly Ala Val Leu Leu Leu Pro Phe Ser Ile Ile Ser Asn Glu
80 85 90
Val Leu Leu Ser Leu Pro Arg Asn Tyr Tyr Ile Gln Trp Leu Asn
95 100 105
Gly Ser Leu Ile His Gly Leu Trp Asn Leu Val Phe Leu Phe Pro
110 115 120
Asn Leu Ser Leu Ile Phe Leu Met Pro Phe Ala Tyr Phe Phe Thr

	125		130		135
Glu Ser Glu Gly	Phe Ala Gly Ser Arg	Lys Gly Val Leu Gly Arg			
	140	145			150
Val Tyr Glu Thr	Val Val Met Leu Met	Leu Leu Thr Leu Leu Val			
	155	160			165
Leu Gly Met Val	Trp Val Ala Ser Ala	Ile Val Asp Lys Asn Lys			
	170	175			180
Ala Asn Arg Glu	Ser Leu Tyr Asp Phe	Trp Glu Tyr Tyr Leu Pro			
	185	190			195
Tyr Leu Tyr Ser	Cys Ile Ser Phe Leu	Gly Val Leu Leu Leu Leu			
	200	205			210
Val Cys Thr Pro	Leu Gly Leu Ala Arg	Met Phe Ser Val Thr Gly			
	215	220			225
Lys Leu Leu Val	Lys Pro Arg Leu Leu	Glu Asp Leu Glu Glu Gln			
	230	235			240
Leu Tyr Cys Ser	Ala Phe Glu Glu Ala	Ala Leu Thr Arg Arg Ile			
	245	250			255
Cys Asn Pro Thr	Ser Cys Trp Leu Pro	Leu Asp Met Glu Leu Leu			
	260	265			270
His Arg Gln Val	Leu Ala Leu Gln Thr	Gln Arg Val Leu Leu Glu			
	275	280			285
Lys Arg Arg Lys	Ala Ser Ala Trp Gln	Arg Asn Leu Gly Tyr Pro			
	290	295			300
Leu Ala Met Leu	Cys Leu Leu Val Leu	Thr Gly Leu Ser Val Leu			
	305	310			315
Ile Val Ala Ile	His Ile Leu Glu Leu	Leu Ile Asp Glu Ala Ala			
	320	325			330
Met Pro Arg Gly	Met Gln Gly Thr Ser	Leu Gly Gln Val Ser Phe			
	335	340			345
Ser Lys Leu Gly	Ser Phe Gly Ala Val	Ile Gln Val Val Leu Ile			
	350	355			360
Phe Tyr Leu Met	Val Ser Ser Val Val	Gly Phe Tyr Ser Ser Pro			
	365	370			375
Leu Phe Arg Ser	Leu Arg Pro Arg Trp	His Asp Thr Ala Met Thr			
	380	385			390
Gln Ile Ile Gly	Asn Cys Val Cys Leu	Leu Val Leu Ser Ser Ala			
	395	400			405
Leu Pro Val Phe	Ser Arg Thr Leu Gly	Leu Thr Arg Phe Asp Leu			
	410	415			420
Leu Gly Asp Phe	Gly Arg Phe Asn Trp	Leu Gly Asn Phe Tyr Ile			
	425	430			435
Val Phe Leu Tyr	Asn Ala Ala Phe Ala	Gly Leu Thr Thr Leu Cys			

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catcagcaat gaggtgctgc actccc 526

<210> 141
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 141
gactgtatct gagccccaga ctgc 24

<210> 142
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 142
tcagcaatga ggtgctgctc 20

<210> 143
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 143
tgaggaagat gagggacagg ttgg 24

<210> 144
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 144
tatggaagca cctgactacg aagtgctatc cgtgcgagaa cagctattcc 50

<210> 145
<211> 685
<212> DNA
<213> Homo sapiens

<400> 145
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tggtccaggt cttcatgctg ctgtgggtga tattactggt cctggctcct 150
gtcagtggac agtttgcaag gacaccacagg cccattatct tcctccagcc 200
tccatggacc acagtcttcc aaggagagag agtgaccctc acttgcaagg 250

gatttcgctt ctactcacca cagaaaacaa aatggtacca tcggtacctt 300
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 atctggagag tacagatgcc agggccaggg ctcccctctc agtagccctg 400
 tgcacttgga tttttcttca gagatgggat ttccatcatgc tgcccaggct 450
 aatgttgaac tcctgggctc aagtgatctg ctcacctagg cctctcaaag 500
 cgctgggatt acagcttcgc tgatcctgca agctccactt tctgtgtttg 550
 aaggagactc tgtggttctg aggtgccggg caaaggcgga agtaacactg 600
 aataatacta tttaacaaga tgataatgtc ctggcattcc ttaataaaag 650
 aactgacttc caaaaaaaaa aaaaaaaaaa aaaaa 685

<210> 146
 <211> 124
 <212> PRT
 <213> Homo sapiens

<400> 146
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 Gln Phe Ala Arg Thr Pro Arg Pro Ile Ile Phe Leu Gln Pro Pro
 20 25 30
 Trp Thr Thr Val Phe Gln Gly Glu Arg Val Thr Leu Thr Cys Lys
 35 40 45
 Gly Phe Arg Phe Tyr Ser Pro Gln Lys Thr Lys Trp Tyr His Arg
 50 55 60
 Tyr Leu Gly Lys Glu Ile Leu Arg Glu Thr Pro Asp Asn Ile Leu
 65 70 75
 Glu Val Gln Glu Ser Gly Glu Tyr Arg Cys Gln Ala Gln Gly Ser
 80 85 90
 Pro Leu Ser Ser Pro Val His Leu Asp Phe Ser Ser Glu Met Gly
 95 100 105
 Phe Pro His Ala Ala Gln Ala Asn Val Glu Leu Leu Gly Ser Ser
 110 115 120

Asp Leu Leu Thr

<210> 147
 <211> 1621
 <212> DNA
 <213> Homo sapiens

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 cccccccggt gtgaggcggc ctcacagggc cgggtgggct ggcgagccga 100
 cgcggcggcg gaggaggctg tgaggagtgt gtggaacagg acccgggaca 150

gaggaacccat ggctccgcag aacctgagca ccttttgcct gttgctgcta 200
 tacctcatcg gggcggtgat tgccggacga gatttctata agatcttggg 250
 ggtgcctcga agtgcctcta taaaggatat taaaaaggcc tataggaaac 300
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 gagaaattcc aggatctggg tgctgcttat gaggttctgt cagatagtga 400
 gaaacggaaa cagtacgata cttatggtga agaaggatta aaagatggtc 450
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 ttcatgtttg gaggaacccc tcgtcagcaa gacagaaata ttccaagagg 550
 aagtgatatt attgtagatc tagaagtcac tttggaagaa gtatatgcag 600
 gaaattttgt ggaagtagtt agaaacaaac ctgtggcaag gcaggctcct 650
 ggcaaacgga agtgcaattg tcggcaagag atgcggacca cccagctggg 700
 ccctgggccc ttccaaatga cccaggaggt ggtctgcgac gaatgcccta 750
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 ggggtgagag acggcatgga gtaccctttt attggagaag gtgagcctca 850
 cgtggatggg gagcctggag atttacggtt ccgaatcaaa gttgtcaagc 900
 acccaatatt tgaaaggaga ggagatgatt tgtacacaaa tgtgacaatc 950
 tcattagtgt agtcactggt tggctttgag atggatatta ctcaattgga 1000
 tggtcacaag gtacatattt cccgggataa gatcaccagg ccaggagcga 1050
 agctatggaa gaaaggggaa gggctcccca actttgacaa caacaatata 1100
 aagggtcttt tgataatcac ttttgatgtg gattttccaa aagaacagtt 1150
 aacagaggaa gcgagagaag gtatcaaaca gctactgaaa caagggtcag 1200
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 tttttatcta atgatcatca tgaaatgaat aagagggctt aagaatttgt 1400
 ccatttgcat tcggaaaaga atgaccagca aaaggtttac taataoctct 1450
 ccctttgggg atttaatgtc tgggtgctgcc gcctgagttt caagaattaa 1500
 agctgcaaga ggactccagg agcaaaagaa acacaatata gagggttgga 1550
 gttgttagca atttcattca aaatgccaac tggagaagtc tgtttttaaa 1600
 tacattttgt tgttattttt a 1621

<210> 148
 <211> 358
 <212> PRT

Variable	Mean	SD	Min	Max
Age	35.5	10.5	18	65
Gender	Male	10.5	0	21
Marital status	Married	10.5	0	21
Education	High school	10.5	0	21
Occupation	Unemployed	10.5	0	21
Income	Low	10.5	0	21
Health status	Good	10.5	0	21
Smoking status	Non-smoker	10.5	0	21
Alcohol consumption	Non-drinker	10.5	0	21
Exercise frequency	Low	10.5	0	21
Stress level	Low	10.5	0	21
Sleep quality	Good	10.5	0	21
Appetite	Good	10.5	0	21
Weight change	Stable	10.5	0	21
Blood pressure	Normal	10.5	0	21
Blood sugar	Normal	10.5	0	21
Cholesterol	Normal	10.5	0	21
Triglycerides	Normal	10.5	0	21
Hemoglobin A1c	Normal	10.5	0	21
Hemoglobin	Normal	10.5	0	21
White blood cells	Normal	10.5	0	21
Platelets	Normal	10.5	0	21
Red blood cells	Normal	10.5	0	21
Hematocrit	Normal	10.5	0	21
Hemoglobin	Normal	10.5	0	21
White blood cells	Normal	10.5	0	21
Platelets	Normal	10.5	0	21
Red blood cells	Normal	10.5	0	21
Hematocrit	Normal	10.5	0	21
Hemoglobin	Normal	10.5	0	21
White blood cells	Normal	10.5	0	21
Platelets	Normal	10.5	0	21
Red blood cells	Normal	10.5	0	21
Hematocrit	Normal	10.5	0	21
Hemoglobin	Normal	10.5	0	21
White blood cells	Normal	10.5	0	21
Platelets	Normal	10.5	0	21
Red blood cells	Normal	10.5	0	21
Hematocrit	Normal	10.5	0	21
Hemoglobin	Normal	10.5	0	21
White blood cells	Normal	10.5	0	21
Platelets	Normal	10.5	0	21
Red blood cells	Normal	10.5	0	21
Hematocrit	Normal	10.5	0	21
Hemoglobin	Normal	10.5	0	21
White blood cells	Normal	10.5	0	21
Platelets	Normal	10.5	0	21
Red blood cells	Normal	10.5	0	21
Hematocrit	Normal	10.5	0	21
Hemoglobin	Normal	10.5	0	21
White blood cells	Normal	10.5	0	21
Platelets	Normal	10.5	0	21
Red blood cells	Normal	10.5	0	21
Hematocrit	Normal	10.5	0	21
Hemoglobin	Normal	10.5	0	21
White blood cells	Normal	10.5	0	21
Platelets	Normal	10.5	0	21
Red blood cells	Normal	10.5	0	21
Hematocrit	Normal	10.5	0	21
Hemoglobin	Normal	10.5	0	21
White blood cells	Normal	10.5	0	21
Platelets	Normal	10.5	0	21
Red blood cells	Normal	10.5	0	21
Hematocrit	Normal	10.5	0	21
Hemoglobin	Normal	10.5	0	21
White blood cells	Normal	10.5	0	21
Platelets	Normal	10.5	0	21
Red blood cells	Normal	10.5	0	21
Hematocrit	Normal	10.5	0	21
Hemoglobin	Normal	10.5	0	21
White blood cells	Normal	10.5	0	21
Platelets	Normal	10.5	0	21
Red blood cells	Normal	10.5	0	21
Hematocrit	Normal	10.5	0	21
Hemoglobin	Normal	10.5	0	21
White blood cells	Normal	10.5	0	21
Platelets	Normal	10.5	0	21
Red blood cells	Normal	10.5	0	21
Hematocrit	Normal	10.5	0	21
Hemoglobin	Normal	10.5	0	21
White blood cells	Normal	10.5	0	21
Platelets	Normal	10.5	0	21
Red blood cells	Normal	10.5	0	21
Hematocrit	Normal	10.5	0	21
Hemoglobin	Normal	10.5	0	

Met	Ala	Pro	Gln	Asn	Leu	Ser	Thr	Phe	Cys	Leu	Leu	Leu	Leu	Tyr
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Leu	Ile	Gly	Ala	Val	Ile	Ala	Gly	Arg	Asp	Phe	Tyr	Lys	Ile	Leu
				20					25					30
Gly	Val	Pro	Arg	Ser	Ala	Ser	Ile	Lys	Asp	Ile	Lys	Lys	Ala	Tyr
				35					40					45
Arg	Lys	Leu	Ala	Leu	Gln	Leu	His	Pro	Asp	Arg	Asn	Pro	Asp	Asp
				50					55					60
Pro	Gln	Ala	Gln	Glu	Lys	Phe	Gln	Asp	Leu	Gly	Ala	Ala	Tyr	Glu
				65					70					75
Val	Leu	Ser	Asp	Ser	Glu	Lys	Arg	Lys	Gln	Tyr	Asp	Thr	Tyr	Gly
				80					85					90
Glu	Glu	Gly	Leu	Lys	Asp	Gly	His	Gln	Ser	Ser	His	Gly	Asp	Ile
				95					100					105
Phe	Ser	His	Phe	Phe	Gly	Asp	Phe	Gly	Phe	Met	Phe	Gly	Gly	Thr
				110					115					120
Pro	Arg	Gln	Gln	Asp	Arg	Asn	Ile	Pro	Arg	Gly	Ser	Asp	Ile	Ile
				125					130					135
Val	Asp	Leu	Glu	Val	Thr	Leu	Glu	Glu	Val	Tyr	Ala	Gly	Asn	Phe
				140					145					150
Val	Glu	Val	Val	Arg	Asn	Lys	Pro	Val	Ala	Arg	Gln	Ala	Pro	Gly
				155					160					165
Lys	Arg	Lys	Cys	Asn	Cys	Arg	Gln	Glu	Met	Arg	Thr	Thr	Gln	Leu
				170					175					180
Gly	Pro	Gly	Arg	Phe	Gln	Met	Thr	Gln	Glu	Val	Val	Cys	Asp	Glu
				185					190					195
Cys	Pro	Asn	Val	Lys	Leu	Val	Asn	Glu	Glu	Arg	Thr	Leu	Glu	Val
				200					205					210
Glu	Ile	Glu	Pro	Gly	Val	Arg	Asp	Gly	Met	Glu	Tyr	Pro	Phe	Ile
				215					220					225
Gly	Glu	Gly	Glu	Pro	His	Val	Asp	Gly	Glu	Pro	Gly	Asp	Leu	Arg
				230					235					240
Phe	Arg	Ile	Lys	Val	Val	Lys	His	Pro	Ile	Phe	Glu	Arg	Arg	Gly
				245					250					255
Asp	Asp	Leu	Tyr	Thr	Asn	Val	Thr	Ile	Ser	Leu	Val	Glu	Ser	Leu
				260					265					270
Val	Gly	Phe	Glu	Met	Asp	Ile	Thr	His	Leu	Asp	Gly	His	Lys	Val
				275					280					285
His	Ile	Ser	Arg	Asp	Lys	Ile	Thr	Arg	Pro	Gly	Ala	Lys	Leu	Trp
				290					295					300

Lys Lys Gly Glu Gly Leu Pro Asn Phe Asp Asn Asn Asn Ile Lys
 305 310 315

Gly Ser Leu Ile Ile Thr Phe Asp Val Asp Phe Pro Lys Glu Gln
 320 325 330

Leu Thr Glu Glu Ala Arg Glu Gly Ile Lys Gln Leu Leu Lys Gln
 335 340 345

Gly Ser Val Gln Lys Val Tyr Asn Gly Leu Gln Gly Tyr
 350 355

<210> 149
 <211> 509
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 34, 52, 134, 142, 155, 158, 196, 217, 228, 272, 347, 410, 445,
 482
 <223> unknown base

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 gaccgggaca gaggaaccat ggttccgcag aacntgagca cnttttgct 150
 gttgntgnta tacttcatcg gggcggtgat tgccggacga gatttntata 200
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 acaagcccag gagaaattcc aggatttggg tgctgcttat gaggttntgt 350
 cagatagtga gaaacggaaa cagtacgata attatggtga agaaggatta 400
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 <211> 1532
 <212> DNA
 <213> Homo sapiens

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 ctcttcccca atttgccact tccagcagct ttagcccatg aggaggatgt 150
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 gttgccatag gtgtgctggc caccatcttt ctggcttcgt ttgcagcctt 250
 ggtgctggtt tgcaggcagc gctactgccg gccgcgagac ctgctgcagc 300

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 aaggaatgcc tgccatctga cgggaggcct ggactggatt gaccagtctc 750
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 ctgatctgca ttttcagaag aggacaatca attgaaacta agtagggggt 1300
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 atacttatgt ttccctcaaa aaaaaaaaaa aa 1532

<210> 151

<211> 226

<212> PRT

<213> Homo sapiens

<400> 151

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Phe	Leu	Ala	Ser	Phe	Ala	Ala	Leu	Val	Leu	Val	Cys	Arg	Gln	Arg
				20					25					30

Tyr	Cys	Arg	Pro	Arg	Asp	Leu	Leu	Gln	Arg	Tyr	Asp	Ser	Lys	Pro
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

	35		40		45
Ile Val Asp Leu	Ile Gly Ala Met Glu Thr Gln Ser Glu Pro Ser				
	50		55		60
Glu Leu Glu Leu Asp	Asp Val Val Ile Thr Asn Pro His Ile Glu				
	65		70		75
Ala Ile Leu Glu Asn	Glu Asp Trp Ile Glu Asp Ala Ser Gly Leu				
	80		85		90
Met Ser His Cys Ile	Ala Ile Leu Lys Ile Cys His Thr Leu Thr				
	95		100		105
Glu Lys Leu Val Ala	Met Thr Met Gly Ser Gly Ala Lys Met Lys				
	110		115		120
Thr Ser Ala Ser Val	Ser Asp Ile Ile Val Val Ala Lys Arg Ile				
	125		130		135
Ser Pro Arg Val Asp	Asp Val Val Lys Ser Met Tyr Pro Pro Leu				
	140		145		150
Asp Pro Lys Leu Leu	Asp Ala Arg Thr Thr Ala Leu Leu Leu Ser				
	155		160		165
Val Ser His Leu Val	Leu Val Thr Arg Asn Ala Cys His Leu Thr				
	170		175		180
Gly Gly Leu Asp Trp	Ile Asp Gln Ser Leu Ser Ala Ala Glu Glu				
	185		190		195
His Leu Glu Val Leu	Arg Glu Ala Ala Leu Ala Ser Glu Pro Asp				
	200		205		210
Lys Gly Leu Pro Gly	Pro Glu Gly Phe Leu Gln Glu Gln Ser Ala				
	215		220		225

Ile

<210> 152
 <211> 1027
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 1017, 1020
 <223> unknown base

<400> 152
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 aaaattggaa tgggattaac aggatttggga gtgtttttcc tgttcttttg 150
 aatgattctc ttttttgaca aagcactact ggctatttga aatgttttat 200
 ttgtagccgg ottggctttt gtaattgggt tagaaagaac attcagattc 250
 ttcttccaaa aacataaaat gaaagctaca gggttttttc tgggtggtgt 300

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 attagaagag tgccagtcct tggatccctc ctaaatttac ctggaattag 450
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 ttagagaact gtggtgcctg tttcttttct ttttattttg aaggctcagg 850
 agcatccata ggcatttgct ttttagaagt gtccactgca atggcaaaaa 900
 tatttccagt tgcactgtat ctctggaagt gatgcatgaa ttcgattgga 950
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 ggattacttt tttttgngcn cagggcc 1027

<210> 153
 <211> 138
 <212> PRT
 <213> Homo sapiens

<220>
 <221> N-myristoylation Sites
 <222> 11-16, 51-56 and 116-121
 <223> N-myristoylation Sites.

<220>
 <221> Transmembrane domains
 <222> 12-30, 33-52, 69-89 and 93-109
 <223> Transmembrane domains

<220>
 <221> Aminoacyl-transfer RNA Synthetases.
 <222> 49-59
 <223> Aminoacyl-transfer RNA synthetases class-II protein.

<400> 153
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 Asp Lys Ala Leu Leu Ala Ile Gly Asn Val Leu Phe Val Ala Gly
 35 40 45
 Leu Ala Phe Val Ile Gly Leu Glu Arg Thr Phe Arg Phe Phe Phe
 50 55 60

Gln Lys His Lys Met Lys Ala Thr Gly Phe Phe Leu Gly Gly Val
65 70 75
Phe Val Val Leu Ile Gly Trp Pro Leu Ile Gly Met Ile Phe Glu
80 85 90
Ile Tyr Gly Phe Phe Leu Leu Phe Arg Gly Phe Phe Pro Val Val
95 100 105
Val Gly Phe Ile Arg Arg Val Pro Val Leu Gly Ser Leu Leu Asn
110 115 120
Leu Pro Gly Ile Arg Ser Phe Val Asp Lys Val Gly Glu Ser Asn
125 130 135
Asn Met Val

<210> 154
<211> 405
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 66
<223> unknown base

<400> 154
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actcagcttc ccacntggg ctttccgagg tgctttcgcc gctgtcccca 100
ccactgcagc catgatctcc ttaacggaca cgcagaaaat tggaatggga 150
ttaaccggat ttggagtgtt tttcctgttc tttggaatga ttctcttttt 200
tgacaaagca ctactggcta ttggaaatgt tttatttgta gccggcttgg 250
cttttgtaat tggtttagaa agaacattca gattcttctt ccaaaaacat 300
aaaatgaaag ctacaggttt ttttctgggt ggtgtatttg tagtccttat 350
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tggtc 405

<210> 155
<211> 1781
<212> DNA
<213> Homo sapiens

<400> 155
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tttcttctt ctggaaatct ttgactgtgg gtagttattt atttctgaat 150
aagagcgtcc acgcatcatg gacctcgcg gactgctgaa gtctcagttc 200
ctgtgccacc tggctttctg ctacgtcttt attgcctcag ggctaatacat 250

caacaccatt cagctcttca ctctcctcct ctggcccatt aacaagcagc 300
 tcttccggaa gatcaactgc agactgtcct attgcatctc aagccagctg 350
 gtgatgctgc tggagtgggtg gtcgggcacg gaatgcacca tcttcacgga 400
 cccgcgcgcc tacctcaagt atgggaagga aaatgccatc gtggttctca 450
 accacaagtt tgaaattgac tttctgtgtg gctggagcct gtccgaacgc 500
 tttgggctgt tagggggctc caaggtcctg gccaaagaa agctggccta 550
 tgtcccaatt atcggctgga tgtggtactt caccgagatg gtcttctgtt 600
 cgcgcaagtg ggagcaggat cgcaagacgg ttgccaccag tttgcagcac 650
 ctccgggact accccgagaa gtattttttc ctgattcact gtgagggcac 700
 acggttcacg gagaagaagc atgagatcag catgcagggtg gcccgggcca 750
 aggggctgcc tcgcctcaag catcacctgt tgccacgaac caagggttc 800
 gccatcacccg tgaggagctt gagaaatgta gtttcagctg tatatgactg 850
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 acggaaagaa ataccatgca gatttgtatg ttaggaggat cccactggaa 950
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 ccaggagaag gatgcctttc aggaggagta ctacaggacg ggcaccttc 1050
 cagagacgcc catggtgccc ccccggcggc cctggaccct cgtgaactgg 1100
 ctgttttggg cctcgtgggt gctctacctt ttcttccagt tcttggtcag 1150
 catgatcagg agcgggtctt ccctgacgct ggccagcttc atcctcgtct 1200
 tctttgtggc ctccgtggga gttcgatgga tgattggtgt gacggaaatt 1250
 gacaagggtc ctgcctacgg caactctgac agcaagcaga aactgaatga 1300
 ctgactcagg gaggtgtcac catccgaagg gaaccttggg gaactggtgg 1350
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 cctgctgggc acggcggaag tcacgacctc tccagccagg gagtctggtc 1450
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 atcctttggt gctgagtttt ctgtaaccct tggttgccag agataaagtg 1700
 aaaagtgttt taggtgagat gactaaatta tgcctccaag aaaaaaaaaat 1750
 taaagtgttt ttctgggtca aaaaaaaaaa a 1781

<210> 156

<211> 378
 <212> PRT
 <213> Homo sapiens

<400> 156

Met	Asp	Leu	Ala	Gly	Leu	Leu	Lys	Ser	Gln	Phe	Leu	Cys	His	Leu	1	5	10	15
Val	Phe	Cys	Tyr	Val	Phe	Ile	Ala	Ser	Gly	Leu	Ile	Ile	Asn	Thr	20	25	30	
Ile	Gln	Leu	Phe	Thr	Leu	Leu	Leu	Trp	Pro	Ile	Asn	Lys	Gln	Leu	35	40	45	
Phe	Arg	Lys	Ile	Asn	Cys	Arg	Leu	Ser	Tyr	Cys	Ile	Ser	Ser	Gln	50	55	60	
Leu	Val	Met	Leu	Leu	Glu	Trp	Trp	Ser	Gly	Thr	Glu	Cys	Thr	Ile	65	70	75	
Phe	Thr	Asp	Pro	Arg	Ala	Tyr	Leu	Lys	Tyr	Gly	Lys	Glu	Asn	Ala	80	85	90	
Ile	Val	Val	Leu	Asn	His	Lys	Phe	Glu	Ile	Asp	Phe	Leu	Cys	Gly	95	100	105	
Trp	Ser	Leu	Ser	Glu	Arg	Phe	Gly	Leu	Leu	Gly	Gly	Ser	Lys	Val	110	115	120	
Leu	Ala	Lys	Lys	Glu	Leu	Ala	Tyr	Val	Pro	Ile	Ile	Gly	Trp	Met	125	130	135	
Trp	Tyr	Phe	Thr	Glu	Met	Val	Phe	Cys	Ser	Arg	Lys	Trp	Glu	Gln	140	145	150	
Asp	Arg	Lys	Thr	Val	Ala	Thr	Ser	Leu	Gln	His	Leu	Arg	Asp	Tyr	155	160	165	
Pro	Glu	Lys	Tyr	Phe	Phe	Leu	Ile	His	Cys	Glu	Gly	Thr	Arg	Phe	170	175	180	
Thr	Glu	Lys	Lys	His	Glu	Ile	Ser	Met	Gln	Val	Ala	Arg	Ala	Lys	185	190	195	
Gly	Leu	Pro	Arg	Leu	Lys	His	His	Leu	Leu	Pro	Arg	Thr	Lys	Gly	200	205	210	
Phe	Ala	Ile	Thr	Val	Arg	Ser	Leu	Arg	Asn	Val	Val	Ser	Ala	Val	215	220	225	
Tyr	Asp	Cys	Thr	Leu	Asn	Phe	Arg	Asn	Asn	Glu	Asn	Pro	Thr	Leu	230	235	240	
Leu	Gly	Val	Leu	Asn	Gly	Lys	Lys	Tyr	His	Ala	Asp	Leu	Tyr	Val	245	250	255	
Arg	Arg	Ile	Pro	Leu	Glu	Asp	Ile	Pro	Glu	Asp	Asp	Asp	Glu	Cys	260	265	270	
Ser	Ala	Trp	Leu	His	Lys	Leu	Tyr	Gln	Glu	Lys	Asp	Ala	Phe	Gln	275	280	285	
Glu	Glu	Tyr	Tyr	Arg	Thr	Gly	Thr	Phe	Pro	Glu	Thr	Pro	Met	Val				

	290		295		300
Pro Pro Arg Arg	Pro Trp Thr Leu Val	Asn Trp Leu Phe Trp	Ala		
	305	310	315		
Ser Leu Val Leu	Tyr Pro Phe Phe Gln	Phe Leu Val Ser Met	Ile		
	320	325	330		
Arg Ser Gly Ser	Ser Leu Thr Leu Ala	Ser Phe Ile Leu Val	Phe		
	335	340	345		
Phe Val Ala Ser	Val Gly Val Arg Trp	Met Ile Gly Val Thr	Glu		
	350	355	360		
Ile Asp Lys Gly	Ser Ala Tyr Gly Asn	Ser Asp Ser Lys Gln	Lys		
	365	370	375		

Leu Asn Asp

<210> 157
 <211> 1849
 <212> DNA
 <213> Homo sapiens

<400> 157
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 acggaaggtt ttcttcttgg ggaagtaaaa ggtgaagcca agaacagcat 150
 tactgattcc caaatggatg atgttgaagt tgtttatata attgacattc 200
 agaaatatat tccatgctat cagcttttta gcttttataa ttcttcaggc 250
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 tttagagagag gctgcttcac aaaaacttgc aggagcattt ttcaaaccac 400
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 atatgcaaaa aagtggaaga cagtgaacaa gcagtagata aactagtaaa 750
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 gcataaagcc ttagacttag atgacagatg gcaattcaag agatctcggt 1100
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 aaatttgcaa aacatcatct aaaattttaa aaaaaaaaaa aaaaaaaaaa 1849

<210> 158
 <211> 409
 <212> PRT
 <213> Homo sapiens

<400> 158
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 Gly Ala Leu Ala Phe Gln His Leu Asn Thr Asp Ser Asp Thr Glu
 20 25 30
 Gly Phe Leu Leu Gly Glu Val Lys Gly Glu Ala Lys Asn Ser Ile
 35 40 45
 Thr Asp Ser Gln Met Asp Asp Val Glu Val Val Tyr Thr Ile Asp
 50 55 60
 Ile Gln Lys Tyr Ile Pro Cys Tyr Gln Leu Phe Ser Phe Tyr Asn
 65 70 75
 Ser Ser Gly Glu Val Asn Glu Gln Ala Leu Lys Lys Ile Leu Ser
 80 85 90
 Asn Val Lys Lys Asn Val Val Gly Trp Tyr Lys Phe Arg Arg His
 95 100 105

<210> 159
<211> 2651
<212> DNA
<213> Homo sapiens

<400> 159

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 aatttctcgt tccatctctg aaagtgcctt cagtgtctgc ttcagaccac 1600
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 aacagtgtag gtacagaact atagttagtt gtgcatttgt gattttatca 2450
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 c 2651

<210> 160
 <211> 556
 <212> PRT
 <213> Homo sapiens

<400> 160
 Met Ala Arg Phe Gly Leu Pro Ala Leu Leu Cys Thr Leu Ala Val
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 Leu Ser Ala Ala Leu Leu Ala Ala Glu Leu Lys Ser Lys Ser Cys
 20 25 30
 Ser Glu Val Arg Arg Leu Tyr Val Ser Lys Gly Phe Asn Lys Asn

35					40					45				
Asp	Ala	Pro	Leu	His	Glu	Ile	Asn	Gly	Asp	His	Leu	Lys	Ile	Cys
				50					55					60
Pro	Gln	Gly	Ser	Thr	Cys	Cys	Ser	Gln	Glu	Met	Glu	Glu	Lys	Tyr
				65					70					75
Ser	Leu	Gln	Ser	Lys	Asp	Asp	Phe	Lys	Ser	Val	Val	Ser	Glu	Gln
				80					85					90
Cys	Asn	His	Leu	Gln	Ala	Val	Phe	Ala	Ser	Arg	Tyr	Lys	Lys	Phe
				95					100					105
Asp	Glu	Phe	Phe	Lys	Glu	Leu	Leu	Glu	Asn	Ala	Glu	Lys	Ser	Leu
				110					115					120
Asn	Asp	Met	Phe	Val	Lys	Thr	Tyr	Gly	His	Leu	Tyr	Met	Gln	Asn
				125					130					135
Ser	Glu	Leu	Phe	Lys	Asp	Leu	Phe	Val	Glu	Leu	Lys	Arg	Tyr	Tyr
				140					145					150
Val	Val	Gly	Asn	Val	Asn	Leu	Glu	Glu	Met	Leu	Asn	Asp	Phe	Trp
				155					160					165
Ala	Arg	Leu	Leu	Glu	Arg	Met	Phe	Arg	Leu	Val	Asn	Ser	Gln	Tyr
				170					175					180
His	Phe	Thr	Asp	Glu	Tyr	Leu	Glu	Cys	Val	Ser	Lys	Tyr	Thr	Glu
				185					190					195
Gln	Leu	Lys	Pro	Phe	Gly	Asp	Val	Pro	Arg	Lys	Leu	Lys	Leu	Gln
				200					205					210
Val	Thr	Arg	Ala	Phe	Val	Ala	Ala	Arg	Thr	Phe	Ala	Gln	Gly	Leu
				215					220					225
Ala	Val	Ala	Gly	Asp	Val	Val	Ser	Lys	Val	Ser	Val	Val	Asn	Pro
				230					235					240
Thr	Ala	Gln	Cys	Thr	His	Ala	Leu	Leu	Lys	Met	Ile	Tyr	Cys	Ser
				245					250					255
His	Cys	Arg	Gly	Leu	Val	Thr	Val	Lys	Pro	Cys	Tyr	Asn	Tyr	Cys
				260					265					270
Ser	Asn	Ile	Met	Arg	Gly	Cys	Leu	Ala	Asn	Gln	Gly	Asp	Leu	Asp
				275					280					285
Phe	Glu	Trp	Asn	Asn	Phe	Ile	Asp	Ala	Met	Leu	Met	Val	Ala	Glu
				290					295					300
Arg	Leu	Glu	Gly	Pro	Phe	Asn	Ile	Glu	Ser	Val	Met	Asp	Pro	Ile
				305					310					315
Asp	Val	Lys	Ile	Ser	Asp	Ala	Ile	Met	Asn	Met	Gln	Asp	Asn	Ser
				320					325					330
Val	Gln	Val	Ser	Gln	Lys	Val	Phe	Gln	Gly	Cys	Gly	Pro	Pro	Lys
				335					340					345
Pro	Leu	Pro	Ala	Gly	Arg	Ile	Ser	Arg	Ser	Ile	Ser	Glu	Ser	Ala

<400> 162
tcacatcgat gggatccatg accg 24

<210> 163
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 163
ggtctcgtga ctgtgaagcc atgttacaac tactgctcaa acatcatgag 50

<210> 164
<211> 870
<212> DNA
<213> Homo sapiens

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Gly Arg Gln Glu Glu Ile Pro Val Val Ile Ala Ala Ser Glu Asp
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Arg Leu Gly Gly Ala Ile Ala Ala Ile Asn Ser Ile Gln His Asn
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Ala Asp His Leu Arg Ser Trp Leu Asn Ser Asp Ser Leu Lys Ser
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Thr Phe Ala Arg Phe Tyr Leu Pro Ile Leu Val Pro Ser Ala Lys
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Phe	Asn	Pro	Gly	Val	Phe	Val	Ala	Asn	Leu	Thr	Glu	Trp	Lys	Arg
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<210> 172

<211> 585

<212> DNA

<213> Homo sapiens

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<223> unknown base

<400> 172

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<211> 1866
<212> DNA
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<212> DNA
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Category	Item	Value
General Information	Age	25.0
	Gender	Male
	Height	1.75
	Weight	70.0
	Education	High School
	Occupation	Student
	Marital Status	Single
	Religion	Christian
	Political Affiliation	Democrat
	Income	\$15,000
Health Status	Current Health	Good
	Chronic Conditions	None
	Recent Illnesses	Flu (2023)
	Stress Level	Low
	Sleep Quality	Good
	Exercise Frequency	3 times/week
	Dietary Habits	Healthy
	Alcohol Consumption	Occasional
	Tobacco Use	Never
	Family History	Heart Disease
Mental Health	Current Mood	Happy
	Stress Management	Good
	Depression Symptoms	None
	Anxiety Level	Low
	Self-Esteem	High
	Life Satisfaction	High
	Resilience	High
	Emotional Stability	High
	Social Support	Strong
	Future Outlook	Optimistic
Social Life	Friends	10
	Family	5
	Community Involvement	Active
	Volunteer Work	Yes
	Travel Frequency	Monthly
	Language Skills	English, Spanish
	Interests	Sports, Music
	Hobbies	Gardening, Reading
	Work-Life Balance	Good

Category	Item	Value
General Information	Age	25.0
	Gender	Male
	Height	1.75
	Weight	70.0
	Education	High School
	Occupation	Student
	Marital Status	Single
	Religion	Christian
	Political Affiliation	Democrat
	Income	\$15,000
Health Status	Current Health	Good
	Chronic Conditions	None
	Recent Illnesses	Flu (2023)
	Stress Level	Low
	Sleep Quality	Good
	Exercise Frequency	3 times/week
	Dietary Habits	Healthy
	Alcohol Consumption	Occasional
	Tobacco Use	Never
	Family History	Heart Disease
Mental Health	Current Mood	Happy
	Stress Management	Good
	Depression Symptoms	None
	Anxiety Level	Low
	Self-Esteem	High
	Life Satisfaction	High
	Resilience	High
	Emotional Stability	High
	Social Support	Strong
	Future Outlook	Optimistic
Social Life	Friends	10
	Family	5
	Community Involvement	Active
	Volunteer Work	Yes
	Travel Frequency	Monthly
	Language Skills	English, Spanish
	Interests	Sports, Music
	Hobbies	Gardening, Reading
	Work-Life Balance	Good

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Category	Item	Value
General Information	Age	25.0
	Gender	Male
	Height	1.75
	Weight	70.0
	Education	High School
	Occupation	Student
	Marital Status	Single
	Religion	Christian
	Political Affiliation	Democrat
	Income	\$15,000
Physical Health	Weight	70.0
	Height	1.75
	Body Mass Index	22.5
	Blood Pressure	120/80
	Heart Rate	75
	Respiratory Rate	18
	Temperature	37.5
	Humidity	60
	Wind Speed	10
	Pressure	1013
Mental Health	Stress Level	High
	Anxiety Level	Medium
	Depression Level	Low
	Anger Level	Low
	Loneliness Level	Medium
	Isolation Level	Low
	Loneliness Level	Medium
	Isolation Level	Low
	Loneliness Level	Medium
	Isolation Level	Low
Social Health	Loneliness Level	Medium
	Isolation Level	Low
	Loneliness Level	Medium
	Isolation Level	Low
	Loneliness Level	Medium
	Isolation Level	Low
	Loneliness Level	Medium
	Isolation Level	Low
	Loneliness Level	Medium
	Isolation Level	Low
Environmental Health	Temperature	37.5
	Humidity	60
	Wind Speed	10
	Pressure	1013
	Weight	70.0
	Height	1.75
	Body Mass Index	22.5
	Blood Pressure	120/80
	Heart Rate	75
	Respiratory Rate	18

Category	Item	Value
General Information	Age	25.0
	Gender	Male
	Height	1.75
	Weight	70.0
	Education	High School
	Occupation	Student
	Marital Status	Single
	Religion	Christian
	Political Affiliation	Democrat
	Income	\$15,000
Health Status	Current Health	Good
	Chronic Conditions	None
	Recent Illnesses	Flu
	Stress Level	Low
	Sleep Quality	Good
	Exercise Frequency	Weekly
	Dietary Habits	Healthy
	Alcohol Consumption	Occasional
	Smoking Status	Non-smoker
	Family History	None
Social Support	Family Size	3
	Close Friends	5
	Community Involvement	Active
	Religious Participation	Regular
	Volunteer Work	Yes
	Work Satisfaction	High
	Life Satisfaction	High
	Overall Well-being	Good
	Future Outlook	Optimistic
	Personal Goals	Graduate

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1997-1998		1998-1999		1999-2000		2000-2001		2001-2002		2002-2003		2003-2004		2004-2005		2005-2006		2006-2007		2007-2008		2008-2009		2009-2010		2010-2011		2011-2012		2012-2013		2013-2014		2014-2015		2015-2016		2016-2017		2017-2018		2018-2019		2019-2020		2020-2021		2021-2022		2022-2023		2023-2024		2024-2025		2025-2026		2026-2027		2027-2028		2028-2029		2029-2030		2030-2031		2031-2032		2032-2033		2033-2034		2034-2035		2035-2036		2036-2037		2037-2038		2038-2039		2039-2040		2040-2041		2041-2042		2042-2043		2043-2044		2044-2045		2045-2046		2046-2047		2047-2048		2048-2049		2049-2050		2050-2051		2051-2052		2052-2053		2053-2054		2054-2055		2055-2056		2056-2057		2057-2058		2058-2059		2059-2060		2060-2061		2061-2062		2062-2063		2063-2064		2064-2065		2065-2066		2066-2067		2067-2068		2068-2069		2069-2070		2070-2071		2071-2072		2072-2073		2073-2074		2074-2075		2075-2076		2076-2077		2077-2078		2078-2079		2079-2080		2080-2081		2081-2082		2082-2083		2083-2084		2084-2085		2085-2086		2086-2087		2087-2088		2088-2089		2089-2090		2090-2091		2091-2092		2092-2093		2093-2094		2094-2095		2095-2096		2096-2097		2097-2098		2098-2099		2099-2100		2100-2101		2101-2102		2102-2103		2103-2104		2104-2105		2105-2106		2106-2107		2107-2108		2108-2109		2109-2110		2110-2111		2111-2112		2112-2113		2113-2114		2114-2115		2115-2116		2116-2117		2117-2118		2118-2119		2119-2120		2120-2121		2121-2122		2122-2123		2123-2124		2124-2125		2125-2126		2126-2127		2127-2128		2128-2129		2129-2130		2130-2131		2131-2132		2132-2133		2133-2134		2134-2135		2135-2136		2136-2137		2137-2138		2138-2139		2139-2140		2140-2141		2141-2142		2142-2143		2143-2144		2144-2145		2145-2146		2146-2147		2147-2148		2148-2149		2149-2150		2150-2151		2151-2152		2152-2153		2153-2154		2154-2155		2155-2156		2156-2157		2157-2158		2158-2159		2159-2160		2160-2161		2161-2162		2162-2163		2163-2164		2164-2165		2165-2166		2166-2167		2167-2168		2168-2169		2169-2170		2170-2171		2171-2172		2172-2173		2173-2174		2174-2175		2175-2176		2176-2177		2177-2178		2178-2179		2179-2180		2180-2181		2181-2182		2182-2183		2183-2184		2184-2185		2185-2186		2186-2187		2187-2188		2188-2189		2189-2190		2190-2191		2191-2192		2192-2193		2193-2194		2194-2195		2195-2196		2196-2197		2197-2198		2198-2199		2199-2200		2200-2201		2201-2202		2202-2203		2203-2204		2204-2205		2205-2206		2206-2207		2207-2208		2208-2209		2209-2210		2210-2211		2211-2212		2212-2213		2213-2214		2214-2215		2215-2216		2216-2217		2217-2218		2218-2219		2219-2220		2220-2221		2221-2222		2222-2223		2223-2224	
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Category	Item	Value
General Information	Age	25.0
	Gender	Male
	Height	1.75
	Weight	70.0
	Education	High School
	Occupation	Student
	Marital Status	Single
	Religion	Christian
	Political Affiliation	Democrat
	Income	\$15,000
Physical Health	Weight	70.0
	Height	1.75
	Body Mass Index	22.5
	Blood Pressure	120/80
	Heart Rate	75
	Respiratory Rate	18
	Temperature	37.5
	Humidity	60
	Wind Speed	10
	Pressure	1013
Mental Health	Stress Level	High
	Anxiety Level	Medium
	Depression Level	Low
	Anger Level	Low
	Loneliness Level	Medium
	Isolation Level	Low
	Loneliness Level	Medium
	Isolation Level	Low
	Loneliness Level	Medium
	Isolation Level	Low
Social Health	Loneliness Level	Medium
	Isolation Level	Low
	Loneliness Level	Medium
	Isolation Level	Low
	Loneliness Level	Medium
	Isolation Level	Low
	Loneliness Level	Medium
	Isolation Level	Low
	Loneliness Level	Medium
	Isolation Level	Low
Environmental Health	Temperature	37.5
	Humidity	60
	Wind Speed	10
	Pressure	1013
	Weight	70.0
	Height	1.75
	Body Mass Index	22.5
	Blood Pressure	120/80
	Heart Rate	75
	Respiratory Rate	18

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1997-1998		1998-1999		1999-2000		2000-2001		2001-2002		2002-2003		2003-2004		2004-2005		2005-2006		2006-2007		2007-2008		2008-2009		2009-2010		2010-2011		2011-2012		2012-2013		2013-2014		2014-2015		2015-2016		2016-2017		2017-2018		2018-2019		2019-2020		2020-2021		2021-2022		2022-2023		2023-2024		2024-2025		2025-2026		2026-2027		2027-2028		2028-2029		2029-2030		2030-2031		2031-2032		2032-2033		2033-2034		2034-2035		2035-2036		2036-2037		2037-2038		2038-2039		2039-2040		2040-2041		2041-2042		2042-2043		2043-2044		2044-2045		2045-2046		2046-2047		2047-2048		2048-2049		2049-2050		2050-2051		2051-2052		2052-2053		2053-2054		2054-2055		2055-2056		2056-2057		2057-2058		2058-2059		2059-2060		2060-2061		2061-2062		2062-2063		2063-2064		2064-2065		2065-2066		2066-2067		2067-2068		2068-2069		2069-2070		2070-2071		2071-2072		2072-2073		2073-2074		2074-2075		2075-2076		2076-2077		2077-2078		2078-2079		2079-2080		2080-2081		2081-2082		2082-2083		2083-2084		2084-2085		2085-2086		2086-2087		2087-2088		2088-2089		2089-2090		2090-2091		2091-2092		2092-2093		2093-2094		2094-2095		2095-2096		2096-2097		2097-2098		2098-2099		2099-2100		2100-2101		2101-2102		2102-2103		2103-2104		2104-2105		2105-2106		2106-2107		2107-2108		2108-2109		2109-2110		2110-2111		2111-2112		2112-2113		2113-2114		2114-2115		2115-2116		2116-2117		2117-2118		2118-2119		2119-2120		2120-2121		2121-2122		2122-2123		2123-2124		2124-2125		2125-2126		2126-2127		2127-2128		2128-2129		2129-2130		2130-2131		2131-2132		2132-2133		2133-2134		2134-2135		2135-2136		2136-2137		2137-2138		2138-2139		2139-2140		2140-2141		2141-2142		2142-2143		2143-2144		2144-2145		2145-2146		2146-2147		2147-2148		2148-2149		2149-2150		2150-2151		2151-2152		2152-2153		2153-2154		2154-2155		2155-2156		2156-2157		2157-2158		2158-2159		2159-2160		2160-2161		2161-2162		2162-2163		2163-2164		2164-2165		2165-2166		2166-2167		2167-2168		2168-2169		2169-2170		2170-2171		2171-2172		2172-2173		2173-2174		2174-2175		2175-2176		2176-2177		2177-2178		2178-2179		2179-2180		2180-2181		2181-2182		2182-2183		2183-2184		2184-2185		2185-2186		2186-2187		2187-2188		2188-2189		2189-2190		2190-2191		2191-2192		2192-2193		2193-2194		2194-2195		2195-2196		2196-2197		2197-2198		2198-2199		2199-2200		2200-2201		2201-2202		2202-2203		2203-2204		2204-2205		2205-2206		2206-2207		2207-2208		2208-2209		2209-2210		2210-2211		2211-2212		2212-2213		2213-2214		2214-2215		2215-2216		2216-2217		2217-2218		2218-2219		2219-2220		2220-2221		2221-2222		2222-2223		2223-2224	
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1990-1991		1991-1992		1992-1993		1993-1994		1994-1995		1995-1996		1996-1997		1997-1998		1998-1999		1999-2000		2000-2001		2001-2002		2002-2003		2003-2004		2004-2005		2005-2006		2006-2007		2007-2008		2008-2009		2009-2010		2010-2011		2011-2012		2012-2013		2013-2014		2014-2015		2015-2016		2016-2017		2017-2018		2018-2019		2019-2020		2020-2021		2021-2022		2022-2023		2023-2024		2024-2025		2025-2026		2026-2027		2027-2028		2028-2029		2029-2030		2030-2031		2031-2032		2032-2033		2033-2034		2034-2035		2035-2036		2036-2037		2037-2038		2038-2039		2039-2040		2040-2041		2041-2042		2042-2043		2043-2044		2044-2045		2045-2046		2046-2047		2047-2048		2048-2049		2049-2050		2050-2051		2051-2052		2052-2053		2053-2054		2054-2055		2055-2056		2056-2057		2057-2058		2058-2059		2059-2060		2060-2061		2061-2062		2062-2063		2063-2064		2064-2065		2065-2066		2066-2067		2067-2068		2068-2069		2069-2070		2070-2071		2071-2072		2072-2073		2073-2074		2074-2075		2075-2076		2076-2077		2077-2078		2078-2079		2079-2080		2080-2081		2081-2082		2082-2083		2083-2084		2084-2085		2085-2086		2086-2087		2087-2088		2088-2089		2089-2090		2090-2091		2091-2092		2092-2093		2093-2094		2094-2095		2095-2096		2096-2097		2097-2098		2098-2099		2099-2100		2100-2101		2101-2102		2102-2103		2103-2104		2104-2105		2105-2106		2106-2107		2107-2108		2108-2109		2109-2110		2110-2111		2111-2112		2112-2113		2113-2114		2114-2115		2115-2116		2116-2117		2117-2118		2118-2119		2119-2120		2120-2121		2121-2122		2122-2123		2123-2124		2124-2125		2125-2126		2126-2127		2127-2128		2128-2129		2129-2130		2130-2131		2131-2132		2132-2133		2133-2134		2134-2135		2135-2136		2136-2137		2137-2138		2138-2139		2139-2140		2140-2141		2141-2142		2142-2143		2143-2144		2144-2145		2145-2146		2146-2147		2147-2148		2148-2149		2149-2150		2150-2151		2151-2152		2152-2153		2153-2154		2154-2155		2155-2156		2156-2157		2157-2158		2158-2159		2159-2160		2160-2161		2161-2162		2162-2163		2163-2164		2164-2165		2165-2166		2166-2167		2167-2168		2168-2169		2169-2170		2170-2171		2171-2172		2172-2173		2173-2174		2174-2175		2175-2176		2176-2177		2177-2178		2178-2179		2179-2180		2180-2181		2181-2182		2182-2183		2183-2184		2184-2185		2185-2186		2186-2187		2187-2188		2188-2189		2189-2190		2190-2191		2191-2192		2192-2193		2193-2194		2194-2195		2195-2196		2196-2197		2197-2198		2198-2199		2199-2200		2200-2201		2201-2202		2202-2203		2203-2204		2204-2205		2205-2206		2206-2207		2207-2208		2208-2209		2209-2210		2210-2211		2211-2212		2212-2213		2213-2214		2214-2215		2215-2216		2216-2217	
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Category	Value
1. General information	
1.1. Name of the project	1.1.1. Project name
1.2. Date of completion	1.2.1. Date of completion
1.3. Location of the project	1.3.1. Location of the project
1.4. Contact person	1.4.1. Contact person
1.5. Other information	1.5.1. Other information
2. Objectives and aims	
2.1. Objectives	2.1.1. Objectives
2.2. Aims	2.2.1. Aims
2.3. Results	2.3.1. Results
2.4. Conclusions	2.4.1. Conclusions
2.5. Recommendations	2.5.1. Recommendations
3. Methodology	
3.1. Methodology	3.1.1. Methodology
3.2. Data collection	3.2.1. Data collection
3.3. Data analysis	3.3.1. Data analysis
3.4. Results	3.4.1. Results
3.5. Conclusions	3.5.1. Conclusions
3.6. Recommendations	3.6.1. Recommendations
4. Discussion	
4.1. Discussion	4.1.1. Discussion
4.2. Conclusions	4.2.1. Conclusions
4.3. Recommendations	4.3.1. Recommendations
4.4. Other information	4.4.1. Other information
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5.3. Other information	5.3.1. Other information
6. Appendix	
6.1. Appendix	6.1.1. Appendix
6.2. Other information	6.2.1. Other information
7. Summary	
7.1. Summary	7.1.1. Summary
7.2. Conclusions	7.2.1. Conclusions
7.3. Recommendations	7.3.1. Recommendations
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8.2. Other information	8.2.1. Other information
9. Glossary	
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9.2. Other information	9.2.1. Other information
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 aaacacacac acacagagtc tctctctata tatacacacg tacacataaa 1550
 tacaccagc acttgcaagg ctagagggaa actggtgaca ctctacagtc 1600
 tgactgattc agtgtttctg gagagcagga cataaatgta tgatgagaat 1650
 gatcaaggac tctacacact ggggtggcttg gagagcccac tttcccagaa 1700
 taatccttga gagaaaagga atcatgggag caatggtgtt gagttcactt 1750
 caagcccaat gccggtgcag aggggaatgg cttagcgagc tctacagtag 1800
 gtgacctgga ggaaggtcac agccacactg aaaatgggat gtgcatgaac 1850
 acggaggatc catgaactac tgtaaagtgt tgacagtgtg tgcacactgc 1900
 agacagcagg tgaaatgtat gtgtgcaatg cgacgagaat gcagaagtca 1950
 gtaacatgtg catgtttgtt gtgctccttt tttctgttgg taaagtacag 2000
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 aaaaaa 2056

<210> 183
 <211> 311
 <212> PRT
 <213> Homo sapiens
 <220>
 <221> Signal peptide
 <222> 1-29
 <223> Signal peptide
 <220>
 <221> N-glycosylation sites
 <222> 40-43, 134-137

<223> N-glycosylation sites.

<220>

<221> Tissue factor proteins homology

<222> 92-119

<223> Tissue factor proteins homology

<220>

<221> Transmembrane domain

<222> 230-255

<223> Transmembrane domain

<220>

<221> Integrins alpha chain protein homology

<222> 232-262

<223> Integrins alpha chain protein homology

<400> 183

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Phe	Met	Trp	Phe	Phe	Tyr	Ala	Leu	Ile	Pro	Cys	Leu	Leu	Thr	Asp
				20					25					30
Glu	Val	Ala	Ile	Leu	Pro	Ala	Pro	Gln	Asn	Leu	Ser	Val	Leu	Ser
				35					40					45
Thr	Asn	Met	Lys	His	Leu	Leu	Met	Trp	Ser	Pro	Val	Ile	Ala	Pro
				50					55					60
Gly	Glu	Thr	Val	Tyr	Tyr	Ser	Val	Glu	Tyr	Gln	Gly	Glu	Tyr	Glu
				65					70					75
Ser	Leu	Tyr	Thr	Ser	His	Ile	Trp	Ile	Pro	Ser	Ser	Trp	Cys	Ser
				80					85					90
Leu	Thr	Glu	Gly	Pro	Glu	Cys	Asp	Val	Thr	Asp	Asp	Ile	Thr	Ala
				95					100					105
Thr	Val	Pro	Tyr	Asn	Leu	Arg	Val	Arg	Ala	Thr	Leu	Gly	Ser	Gln
				110					115					120
Thr	Ser	Ala	Trp	Ser	Ile	Leu	Lys	His	Pro	Phe	Asn	Arg	Asn	Ser
				125					130					135
Thr	Ile	Leu	Thr	Arg	Pro	Gly	Met	Glu	Ile	Thr	Lys	Asp	Gly	Phe
				140					145					150
His	Leu	Val	Ile	Glu	Leu	Glu	Asp	Leu	Gly	Pro	Gln	Phe	Glu	Phe
				155					160					165
Leu	Val	Ala	Tyr	Trp	Arg	Arg	Glu	Pro	Gly	Ala	Glu	Glu	His	Val
				170					175					180
Lys	Met	Val	Arg	Ser	Gly	Gly	Ile	Pro	Val	His	Leu	Glu	Thr	Met
				185					190					195
Glu	Pro	Gly	Ala	Ala	Tyr	Cys	Val	Lys	Ala	Gln	Thr	Phe	Val	Lys
				200					205					210
Ala	Ile	Gly	Arg	Tyr	Ser	Ala	Phe	Ser	Gln	Thr	Glu	Cys	Val	Glu
				215					220					225

Val	Gln	Gly	Glu	Ala	Ile	Pro	Leu	Val	Leu	Ala	Leu	Phe	Ala	Phe
				230					235					240
Val	Gly	Phe	Met	Leu	Ile	Leu	Val	Val	Val	Pro	Leu	Phe	Val	Trp
				245					250					255
Lys	Met	Gly	Arg	Leu	Leu	Gln	Tyr	Ser	Cys	Cys	Pro	Val	Val	Val
				260					265					270
Leu	Pro	Asp	Thr	Leu	Lys	Ile	Thr	Asn	Ser	Pro	Gln	Lys	Leu	Ile
				275					280					285
Ser	Cys	Arg	Arg	Glu	Glu	Val	Asp	Ala	Cys	Ala	Thr	Ala	Val	Met
				290					295					300
Ser	Pro	Glu	Glu	Leu	Leu	Arg	Ala	Trp	Ile	Ser				
				305					310					

<210> 184
 <211> 808
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 654, 711, 748
 <223> unknown base

<400> 184
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 agaatgcttt attttgaaa gaaacaatgt tctaggtcaa actgagtcta 200
 ccaaatgcag actttcacia tggttctaga agaaatctgg acaagtcttt 250
 tcatgtggtt tttctacgca ttgattccat gtttgctcac agatgaagtg 300
 gccattctgc ctgccctca gaacctctct gtactctcaa ccaacatgaa 350
 gcatctcttg atgtggagcc cagtgatcgc gcctggagaa acagtgtact 400
 attctgtcga ataccagggg gactacgaga gcctgtacac gagccacatc 450
 tggatcccca gcagctggtg ctactcact gaaggctcctg agtgtgatgt 500
 cactgatgac atcacggcca ctgtgccata caacctttgt gtcagggcca 550
 cattgggctc acagacctca gcctggagca tcctgaagca tccctttaat 600
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 ttgtggccta ntggaggagg ggcgaacccc ttgcggcgca aggggttngc 750
 gaacccttg cggccgctgg ggtatctctc gagaaaagag aggcccaata 800
 tgaccac 808

<210> 185
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 185
aggcttcgct gcgactagac ctc 23

<210> 186
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 186
ccaggtcggg taaggatggt tgag 24

<210> 187
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 187
tttctacgca ttgattccat gtttgctcac agatgaagtg gccattctgc 50

<210> 188
<211> 1227
<212> DNA
<213> Homo sapiens

<400> 188
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ggcagcggcg tggctgctcc tgtgggctgc ggccctgcgcg cagcaggagc 100
aggacttcta cgacttcaag gcggtcaaca tccggggcaa actggtgtcg 150
ctggagaagt accgcggatc ggtgtccctg gtggtgaatg tggccagcga 200
gtgcggcttc acagaccagc actaccgagc cctgcagcag ctgcagcgag 250
acctgggccc ccaccacttt aacgtgctcg ccttcccctg caaccagttt 300
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cacctacagt gtctcattcc ccatgtttag caagattgca gtcaccggtg 400
ctggtgccca tctgccttc aagtacctgg cccagacttc tgggaaggag 450
cccacctgga acttctggaa gtacctagta gcccagatg gaaagggtgt 500
aggggcttgg gacccaactg tgtcagtgga ggaggtcaga ccccagatca 550
cagcgctcgt gaggaagctc atcctactga agcgagaaga cttataacca 600

ccgcgtctcc tcctccacca cctcatcccg cccacctgtg tggggctgac 650
 caatgcaaac tcaaagtgtg cttcaaaggg agagaccac tgactctcct 700
 tcctttactc ttatgccatt ggtcccatca ttcttgtggg ggaaaaattc 750
 tagtattttg attatttgaa tcttacagca acaaatagga actcctggcc 800
 aatgagagct cttgaccagt gaatcaccag ccgatacgaa cgtcttgcca 850
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 aggcttctgt aaactgggac caatgattac ctcatagggc tgttgtgagg 950
 attaggatga aatacctgtg aaagtgccta ggagtgcca gccaaatagg 1000
 aggcatcaca tgaacatttt ttgcatataa accaaaaaat aacttgttat 1050
 caataaaaac ttgcatccaa catgaatttc cagccgatga taatccaggc 1100
 caaaggttta gttgttgta tttcctctgt attattttct tcattacaaa 1150
 agaaatgcaa gttcattgta acaatccaaa caatacctca cgatataaaa 1200
 taaaaatgaa agtatcctcc tcaaaaa 1227

<210> 189
 <211> 187
 <212> PRT
 <213> Homo sapiens

<400> 189
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 Ala Ala Cys Ala Gln Gln Glu Gln Asp Phe Tyr Asp Phe Lys Ala
 20 25 30
 Val Asn Ile Arg Gly Lys Leu Val Ser Leu Glu Lys Tyr Arg Gly
 35 40 45
 Ser Val Ser Leu Val Val Asn Val Ala Ser Glu Cys Gly Phe Thr
 50 55 60
 Asp Gln His Tyr Arg Ala Leu Gln Gln Leu Gln Arg Asp Leu Gly
 65 70 75
 Pro His His Phe Asn Val Leu Ala Phe Pro Cys Asn Gln Phe Gly
 80 85 90
 Gln Gln Glu Pro Asp Ser Asn Lys Glu Ile Glu Ser Phe Ala Arg
 95 100 105
 Arg Thr Tyr Ser Val Ser Phe Pro Met Phe Ser Lys Ile Ala Val
 110 115 120
 Thr Gly Thr Gly Ala His Pro Ala Phe Lys Tyr Leu Ala Gln Thr
 125 130 135
 Ser Gly Lys Glu Pro Thr Trp Asn Phe Trp Lys Tyr Leu Val Ala
 140 145 150
 Pro Asp Gly Lys Val Val Gly Ala Trp Asp Pro Thr Val Ser Val

aatgtcaagg aattgactga acgaactaag agctcctgga tgggtccggg 2050
aactcgctg ggcacaaggt gccaaaaggc aggcagcctg cccaggccct 2100
ccctcctgtc catccccac attcccctgt ctgtccttgt gatttggcat 2150
aaagagcttc tgttttcttt gaaaaaaaaa aaaaaaa 2187

<210> 194
<211> 615
<212> PRT
<213> Homo sapiens

<400> 194
Met Ala Val Tyr Val Gly Met Leu Arg Leu Gly Arg Leu Cys Ala
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Gly Ser Ser Gly Val Leu Gly Ala Arg Ala Ala Leu Ser Arg Ser
20 25 30
Trp Gln Glu Ala Arg Leu Gln Gly Val Arg Phe Leu Ser Ser Arg
35 40 45
Glu Val Asp Arg Met Val Ser Thr Pro Ile Gly Gly Leu Ser Tyr
50 55 60
Val Gln Gly Cys Thr Lys Lys His Leu Asn Ser Lys Thr Val Gly
65 70 75
Gln Cys Leu Glu Thr Thr Ala Gln Arg Val Pro Glu Arg Glu Ala
80 85 90
Leu Val Val Leu His Glu Asp Val Arg Leu Thr Phe Ala Gln Leu
95 100 105
Lys Glu Glu Val Asp Lys Ala Ala Ser Gly Leu Leu Ser Ile Gly
110 115 120
Leu Cys Lys Gly Asp Arg Leu Gly Met Trp Gly Pro Asn Ser Tyr
125 130 135
Ala Trp Val Leu Met Gln Leu Ala Thr Ala Gln Ala Gly Ile Ile
140 145 150
Leu Val Ser Val Asn Pro Ala Tyr Gln Ala Met Glu Leu Glu Tyr
155 160 165
Val Leu Lys Lys Val Gly Cys Lys Ala Leu Val Phe Pro Lys Gln
170 175 180
Phe Lys Thr Gln Gln Tyr Tyr Asn Val Leu Lys Gln Ile Cys Pro
185 190 195
Glu Val Glu Asn Ala Gln Pro Gly Ala Leu Lys Ser Gln Arg Leu
200 205 210
Pro Asp Leu Thr Thr Val Ile Ser Val Asp Ala Pro Leu Pro Gly
215 220 225
Thr Leu Leu Leu Asp Glu Val Val Ala Ala Gly Ser Thr Arg Gln
230 235 240
His Leu Asp Gln Leu Gln Tyr Asn Gln Gln Phe Leu Ser Cys His

245										250					255				
Asp	Pro	Ile	Asn	Ile	Gln	Phe	Thr	Ser	Gly	Thr	Thr	Gly	Ser	Pro					
				260					265					270					
Lys	Gly	Ala	Thr	Leu	Ser	His	Tyr	Asn	Ile	Val	Asn	Asn	Ser	Asn					
				275					280					285					
Ile	Leu	Gly	Glu	Arg	Leu	Lys	Leu	His	Glu	Lys	Thr	Pro	Glu	Gln					
				290					295					300					
Leu	Arg	Met	Ile	Leu	Pro	Asn	Pro	Leu	Tyr	His	Cys	Leu	Gly	Ser					
				305					310					315					
Val	Ala	Gly	Thr	Met	Met	Cys	Leu	Met	Tyr	Gly	Ala	Thr	Leu	Ile					
				320					325					330					
Leu	Ala	Ser	Pro	Ile	Phe	Asn	Gly	Lys	Lys	Ala	Leu	Glu	Ala	Ile					
				335					340					345					
Ser	Arg	Glu	Arg	Gly	Thr	Phe	Leu	Tyr	Gly	Thr	Pro	Thr	Met	Phe					
				350					355					360					
Val	Asp	Ile	Leu	Asn	Gln	Pro	Asp	Phe	Ser	Ser	Tyr	Asp	Ile	Ser					
				365					370					375					
Thr	Met	Cys	Gly	Gly	Val	Ile	Ala	Gly	Ser	Pro	Ala	Pro	Pro	Glu					
				380					385					390					
Leu	Ile	Arg	Ala	Ile	Ile	Asn	Lys	Ile	Asn	Met	Lys	Asp	Leu	Val					
				395					400					405					
Val	Ala	Tyr	Gly	Thr	Thr	Glu	Asn	Ser	Pro	Val	Thr	Phe	Ala	His					
				410					415					420					
Phe	Pro	Glu	Asp	Thr	Val	Glu	Gln	Lys	Ala	Glu	Ser	Val	Gly	Arg					
				425					430					435					
Ile	Met	Pro	His	Thr	Glu	Ala	Arg	Ile	Met	Asn	Met	Glu	Ala	Gly					
				440					445					450					
Thr	Leu	Ala	Lys	Leu	Asn	Thr	Pro	Gly	Glu	Leu	Cys	Ile	Arg	Gly					
				455					460					465					
Tyr	Cys	Val	Met	Leu	Gly	Tyr	Trp	Gly	Glu	Pro	Gln	Lys	Thr	Glu					
				470					475					480					
Glu	Ala	Val	Asp	Gln	Asp	Lys	Trp	Tyr	Trp	Thr	Gly	Asp	Val	Ala					
				485					490					495					
Thr	Met	Asn	Glu	Gln	Gly	Phe	Cys	Lys	Ile	Val	Gly	Arg	Ser	Lys					
				500					505					510					
Asp	Met	Ile	Ile	Arg	Gly	Gly	Glu	Asn	Ile	Tyr	Pro	Ala	Glu	Leu					
				515					520					525					
Glu	Asp	Phe	Phe	His	Thr	His	Pro	Lys	Val	Gln	Glu	Val	Gln	Val					
				530					535					540					
Val	Gly	Val	Lys	Asp	Asp	Arg	Met	Gly	Glu	Glu	Ile	Cys	Ala	Cys					
				545					550					555					
Ile	Arg	Leu	Lys	Asp	Gly	Glu	Glu	Thr	Thr	Val	Glu	Glu	Ile	Lys					

560	565	570
Ala Phe Cys Lys Gly Lys Ile Ser His Phe Lys Ile Pro Lys Tyr		
575	580	585
Ile Val Phe Val Thr Asn Tyr Pro Leu Thr Ile Ser Gly Lys Ile		
590	595	600
Gln Lys Phe Lys Leu Arg Glu Gln Met Glu Arg His Leu Asn Leu		
605	610	615

<210> 195
 <211> 642
 <212> DNA
 <213> Homo sapiens

<400> 195
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 agcagttgcg gatgatcctg cccaaccccc tgtaccattg cctgggttcc 100
 gtggcaggca caatgatgtg tctgatgtac ggtgccaccc tcatcctggc 150
 ctctcccatc ttcaatggca agaaggcact ggaggccatc agcagagaga 200
 gaggcacctt cctgtatggt acccccacga tggtcgtgga cattctgaac 250
 cagccagact tctccagtta tgacatctcg accatgtgtg gaggtgtcat 300
 tgctgggtcc cctgcacctc cagagttgat ccgagccatc atcaacaaga 350
 taaatatgaa ggacctggtg gttgcttatg gaaccacaga gaacagtccc 400
 gtgacattcg cgcacttccc tgaggacact gtggagcaga aggcagaaag 450
 cgtgggcaga attatgcctc acacggaggc gcggatcatg aacatggagg 500
 cagggacgct ggcaaagctg aacacgcccg gggagctgtg catccgaggg 550
 tactgcgtca tgctgggcta ctgggggtgag cctcagaaga cagaggaagc 600
 agtggatcag gacaagtggg attggacagg agatgtcgcc ac 642

<210> 196
 <211> 1575
 <212> DNA
 <213> Homo sapiens

<400> 196
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 aggccctgga gtgctacagc tgcgtgcaga aagcagatga cggatgctcc 150
 ccgaacaaga tgaagacagt gaagtgcgcg ccgggctggtg acgtctgcac 200
 cgaggccgtg ggggctggtg agaccatcca cggacaattc tcgctggcag 250
 tgcggggttg cggttcggga ctccccggca agaataaccg cggcctggat 300
 cttcacgggc ttctggcggt catccagctg cagcaatgcg ctcaggatcg 350

ctgcaacgcc aagctcaacc tcacctcgcg ggcgctcgac ccggcaggta 400
atgagagtgc ataccgccc aacggcgtgg agtgctacag ctgtgtgggc 450
ctgagccggg aggcgtgcca gggtagatcg ccgcccgtcg tgagctgcta 500
caacgccagc gatcatgtct acaagggtg cttagacggc aacgtcacct 550
tgacggcagc taatgtgact gtgtccttgc ctgtccgggg ctgtgtccag 600
gatgaattct gcactcggga tggagtaaca ggcccagggt tcacgctcag 650
tggctcctgt tgccaggggt cccgctgtaa ctctgacctc cgcaacaaga 700
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cccacgactg tggcctcaac cacatctgtc accacttcta cctcggcccc 800
agttagaccc acatccacca ccaaaccat gccagcgcca accagtcaga 850
ctccgagaca gggagtagaa cacgaggcct cccgggatga ggagcccagg 900
ttgactggag gcgcccgtgg ccaccaggac cgcagcaatt cagggcagta 950
tcctgcaaaa gggggggccc agcagcccca taataaaggc tgtgtggctc 1000
ccacagctgg attggcagcc cttctgttgg ccgtggctgc tgggtgtcta 1050
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ccaattogcc ctatagttag tcgta 1575

<210> 197
<211> 346
<212> PRT
<213> Homo sapiens

<400> 197
Met Asp Pro Ala Arg Lys Ala Gly Ala Gln Ala Met Ile Trp Thr
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Ala Gly Trp Leu Leu Leu Leu Leu Arg Gly Gly Ala Gln Ala
20 25 30
Leu Glu Cys Tyr Ser Cys Val Gln Lys Ala Asp Asp Gly Cys Ser

[illegible]

<210> 198
<211> 1657
<212> DNA
<213> Homo sapiens

<400> 198
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gtcctggcca gtgcagctga aaaggagaag gaaatggacc cttttcatta 150
tgattaccag accctgagga ttgggggact ggtgttcgct gtggtcctct 200
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tctcttagca actggagata caaagcaagg agctggtgag ccagcgttg 1000
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cctgcttctg agacttcaat ctacagccca gctcatccag atgcagacta 1250
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ccgttggggc cagcacaccg ggatggatgg agggagagca gaggcctttg 1350
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ctttgctctg cctgtcgggtg gtcagagcgg tgagcgaggt gggttggaga 1450
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aacgagagtg ggaactcaac ccagatcccg cccctcctgt cctctgtgtt 1550
cccgcggaac ccaaccaaac cgtgcgctgt gacccattgc tgttctctgt 1600
atcgtgatct atcctcaaca acaacagaaa aaaggaataa aatatccttt 1650
gtttcct 1657

<210> 199
<211> 120
<212> PRT
<213> Homo sapiens

<400> 199
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Val Leu Ala Ser Ala Ala Glu Lys Glu Lys Glu Met Asp Pro Phe
20 25 30
His Tyr Asp Tyr Gln Thr Leu Arg Ile Gly Gly Leu Val Phe Ala
35 40 45
Val Val Leu Phe Ser Val Gly Ile Leu Leu Ile Leu Ser Arg Arg
50 55 60
Cys Lys Cys Ser Phe Asn Gln Lys Pro Arg Ala Pro Gly Asp Glu
65 70 75
Glu Ala Gln Val Glu Asn Leu Ile Thr Ala Asn Ala Thr Glu Pro
80 85 90
Gln Lys Gln Arg Thr Glu Val Gln Pro Ser Gly Gly Ser Leu Trp
95 100 105
Asn Leu Arg Arg Leu Leu Glu Pro Leu Asp Ala Asn Val Asp Ala
110 115 120

<210> 200
<211> 415
<212> DNA
<213> Homo sapiens

<400> 200
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cctcctgggtg ctccactctg cccagggagc caccctgggt ggtcctgagg 100
aagaaagcac cattgagaat tatgcgtcac gacccgaggc ctttaacacc 150
ccgttcctga acatcgacaa attgcgatct gcgtttaagg ctgatgagtt 200
cctgaactgg cagccctct ttgagtctat caaaaggaaa cttcctttcc 250
tcaactggga tgcctttcct aagctgaaag gactgaggag cgcaactcct 300
gatgccagat gaccatgacc tccactggaa gagggggcta gcgtgagcgc 350
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cattttccat ccaaa 415

<210> 201

<211> 99

<212> PRT

<213> Homo sapiens

<400> 201

Met Lys Ile Pro Val Leu Pro Ala Val Val Leu Leu Ser Leu Leu
1 5 10 15

Val Leu His Ser Ala Gln Gly Ala Thr Leu Gly Gly Pro Glu Glu
20 25 30

Glu Ser Thr Ile Glu Asn Tyr Ala Ser Arg Pro Glu Ala Phe Asn
35 40 45

Thr Pro Phe Leu Asn Ile Asp Lys Leu Arg Ser Ala Phe Lys Ala
50 55 60

Asp Glu Phe Leu Asn Trp His Ala Leu Phe Glu Ser Ile Lys Arg
65 70 75

Lys Leu Pro Phe Leu Asn Trp Asp Ala Phe Pro Lys Leu Lys Gly
80 85 90

Leu Arg Ser Ala Thr Pro Asp Ala Gln
95

<210> 202

<211> 678

<212> DNA

<213> Homo sapiens

<400> 202

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cagcaggagt ctcccagggt gttcttctcc agccagttcc aactcaggag 150

acaggtccca aggccatggg agatctctcc tgtggctttg cgggccactc 200

atgagagtgt ttttgtgtaa agtatttttt agaatactgt tgacttcttc 250

atgatttaat aaccatcctt tgcgaagttt tatgaggctt taggggaatg 300

tcaaccctca aatttttggt atactagatg gcttccattt acccaccact 350

attttaaggt ccctttatct ttaggttcaa gggttcattg acttgagaaa 400

gtgcccttct gcagcttcat tgattttggt tatcttcact attaattgta 450

acgattaaaa aagaataaga gcacgcagac ctctaggaga atattttatc 500

cctgggtgcc cctgacacat ttatgtagtg atcccacaaa tgtgattggt 550

aatttaaatg ttattctaatt attagtagat tcagttgtga tgtaatatga 600

ataaccagaa tctatttctt aaaagttttg agtatatttt tcaactagat 650

atttgtatag aaagactgaa tagtgatg 678

<210> 203
 <211> 52
 <212> PRT
 <213> Homo sapiens

<400> 203
 Met Gly Val Glu Ile Ala Phe Ala Ser Val Ile Leu Thr Cys Leu
 1 5 10 15
 Ser Leu Leu Ala Ala Gly Val Ser Gln Val Val Leu Leu Gln Pro
 20 25 30
 Val Pro Thr Gln Glu Thr Gly Pro Lys Ala Met Gly Asp Leu Ser
 35 40 45
 Cys Gly Phe Ala Gly His Ser
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<210> 204
 <211> 1917
 <212> DNA
 <213> Homo sapiens

<400> 204
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 agaaggagtc aggttcaaaa tggaaagtat ttattgacca aattaacagg 150
 tctttggaga attacgaacc atgttcaagt caaaactgca gctgctacca 200
 tgggtgcata gaagaggatc taactccttt ccgaggaggc atctccagga 250
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 actaagaaca gactgtaccg ggaaaatgac tgcattgttcc cctcaagggtg 350
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 tggagatggg gatcaatgta cgagattatc ctcagggttcc taaatggatg 450
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 caatttatcc tacaggctct ggacgggtggg acctcttcag agaagatctg 600
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 ctgcaagttt ccggtttaaa cacctcttcc tgtgtggctc acttgttttc 900
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cgagaaggaa aggttatgat caaattattc ccaaatgtt gaaaactgaa 1200
ctatagtagt catcatagga ccatagtcct ctttgtggca acagatctca 1250
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caattggatt tcaggttccc ttttgtgcc ttcatgccct acttcttaat 1900
gcctctctaa agccaaa 1917

<210> 205
<211> 392
<212> PRT
<213> Homo sapiens

<400> 205
Met Glu Trp Trp Ala Ser Ser Pro Leu Arg Leu Trp Leu Leu Leu
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Phe Leu Leu Pro Ser Ala Gln Gly Arg Gln Lys Glu Ser Gly Ser
20 25 30
Lys Trp Lys Val Phe Ile Asp Gln Ile Asn Arg Ser Leu Glu Asn
35 40 45
Tyr Glu Pro Cys Ser Ser Gln Asn Cys Ser Cys Tyr His Gly Val
50 55 60
Ile Glu Glu Asp Leu Thr Pro Phe Arg Gly Gly Ile Ser Arg Lys
65 70 75
Met Met Ala Glu Val Val Arg Arg Lys Leu Gly Thr His Tyr Gln
80 85 90
Ile Thr Lys Asn Arg Leu Tyr Arg Glu Asn Asp Cys Met Phe Pro

	95	100	105
Ser Arg Cys Ser	Gly Val Glu His Phe	Ile Leu Glu Val Ile	Gly
	110	115	120
Arg Leu Pro Asp	Met Glu Met Val Ile	Asn Val Arg Asp Tyr	Pro
	125	130	135
Gln Val Pro Lys	Trp Met Glu Pro Ala	Ile Pro Val Phe Ser	Phe
	140	145	150
Ser Lys Thr Ser	Glu Tyr His Asp Ile	Met Tyr Pro Ala Trp	Thr
	155	160	165
Phe Trp Glu Gly	Gly Pro Ala Val Trp	Pro Ile Tyr Pro Thr	Gly
	170	175	180
Leu Gly Arg Trp	Asp Leu Phe Arg Glu	Asp Leu Val Arg Ser	Ala
	185	190	195
Ala Gln Trp Pro	Trp Lys Lys Lys Asn	Ser Thr Ala Tyr Phe	Arg
	200	205	210
Gly Ser Arg Thr	Ser Pro Glu Arg Asp	Pro Leu Ile Leu Leu	Ser
	215	220	225
Arg Lys Asn Pro	Lys Leu Val Asp Ala	Glu Tyr Thr Lys Asn	Gln
	230	235	240
Ala Trp Lys Ser	Met Lys Asp Thr Leu	Gly Lys Pro Ala Ala	Lys
	245	250	255
Asp Val His Leu	Val Asp His Cys Lys	Tyr Lys Tyr Leu Phe	Asn
	260	265	270
Phe Arg Gly Val	Ala Ala Ser Phe Arg	Phe Lys His Leu Phe	Leu
	275	280	285
Cys Gly Ser Leu	Val Phe His Val Gly	Asp Glu Trp Leu Glu	Phe
	290	295	300
Phe Tyr Pro Gln	Leu Lys Pro Trp Val	His Tyr Ile Pro Val	Lys
	305	310	315
Thr Asp Leu Ser	Asn Val Gln Glu Leu	Leu Gln Phe Val Lys	Ala
	320	325	330
Asn Asp Asp Val	Ala Gln Glu Ile Ala	Glu Arg Gly Ser Gln	Phe
	335	340	345
Ile Arg Asn His	Leu Gln Met Asp Asp	Ile Thr Cys Tyr Trp	Glu
	350	355	360
Asn Leu Leu Ser	Glu Tyr Ser Lys Phe	Leu Ser Tyr Asn Val	Thr
	365	370	375
Arg Arg Lys Gly	Tyr Asp Gln Ile Ile	Pro Lys Met Leu Lys	Thr
	380	385	390

Glu Leu

<210> 206

<211> 1425
<212> DNA
<213> Homo sapiens

<400> 206

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tttacctccc ttcgccact tcttgaggg atcccgaggt ctggtggtcc 150
ggatgcccgc cagggatggc tggctgccct gcaggaccgc agcatccttg 200
ccccctggc atgggatctg gggctcctgc ttctatttgt tgggcagcac 250
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ggctccttcag aggtcactgt atgtggcctg cactgcctg gccttgacgc 350
tggtgatgcg gtactgggag cccataccca aaggccctgt gttgtgggag 400
gctcgggctg agccatgggc cacctgggtg ccgctcctct gctttgtgct 450
ccatgtcatc tcttggtccc tcatctttag catccttctc gtctttgact 500
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aaagtcagcc tttttctaaa aaaa 1425

<210> 207
 <211> 262
 <212> PRT
 <213> Homo sapiens

<400> 207

Met	Ala	Pro	Ala	Leu	Leu	Leu	Ile	Pro	Ala	Ala	Leu	Ala	Ser	Phe
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Ile	Leu	Ala	Phe	Gly	Thr	Gly	Val	Glu	Phe	Val	Arg	Phe	Thr	Ser
				20					25					30
Leu	Arg	Pro	Leu	Leu	Gly	Gly	Ile	Pro	Glu	Ser	Gly	Gly	Pro	Asp
				35					40					45
Ala	Arg	Gln	Gly	Trp	Leu	Ala	Ala	Leu	Gln	Asp	Arg	Ser	Ile	Leu
				50					55					60
Ala	Pro	Leu	Ala	Trp	Asp	Leu	Gly	Leu	Leu	Leu	Leu	Phe	Val	Gly
				65					70					75
Gln	His	Ser	Leu	Met	Ala	Ala	Glu	Arg	Val	Lys	Ala	Trp	Thr	Ser
				80					85					90
Arg	Tyr	Phe	Gly	Val	Leu	Gln	Arg	Ser	Leu	Tyr	Val	Ala	Cys	Thr
				95					100					105
Ala	Leu	Ala	Leu	Gln	Leu	Val	Met	Arg	Tyr	Trp	Glu	Pro	Ile	Pro
				110					115					120
Lys	Gly	Pro	Val	Leu	Trp	Glu	Ala	Arg	Ala	Glu	Pro	Trp	Ala	Thr
				125					130					135
Trp	Val	Pro	Leu	Leu	Cys	Phe	Val	Leu	His	Val	Ile	Ser	Trp	Leu
				140					145					150
Leu	Ile	Phe	Ser	Ile	Leu	Leu	Val	Phe	Asp	Tyr	Ala	Glu	Leu	Met
				155					160					165
Gly	Leu	Lys	Gln	Val	Tyr	Tyr	His	Val	Leu	Gly	Leu	Gly	Glu	Pro
				170					175					180
Leu	Ala	Leu	Lys	Ser	Pro	Arg	Ala	Leu	Arg	Leu	Phe	Ser	His	Leu
				185					190					195
Arg	His	Pro	Val	Cys	Val	Glu	Leu	Leu	Thr	Val	Leu	Trp	Val	Val
				200					205					210
Pro	Thr	Leu	Gly	Thr	Asp	Arg	Leu	Leu	Leu	Ala	Phe	Leu	Leu	Thr
				215					220					225
Leu	Tyr	Leu	Gly	Leu	Ala	His	Gly	Leu	Asp	Gln	Gln	Asp	Leu	Arg
				230					235					240
Tyr	Leu	Arg	Ala	Gln	Leu	Gln	Arg	Lys	Leu	His	Leu	Leu	Ser	Arg
				245					250					255
Pro	Gln	Asp	Gly	Glu	Ala	Glu								
				260										

<210> 208
 <211> 2095
 <212> DNA

<213> Homo sapiens

<400> 208

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ggaggtcagt gtgctggctt acactgaact gaaactcatg aaaaaccag 1450
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gatgatatgt ggaggaatta aatataaagg aattggaggt ttttgctaaa 1550
gaaattaata ggaccaaaca atttgacat gtcattctgt agactagaat 1600
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caagataaaa aggatagtga atcattcttt acatgcaaac attttccagt 1950
tacttaactg atcagtttat tattgatata tcactccatt aatgtaaagt 2000
cataggtcat tattgcatat cagtaatctc ttggactttg ttaaataattt 2050
tactgtggta atatagagaa gaattaaagc aagaaaatct gaaaa 2095

<210> 209
<211> 331
<212> PRT
<213> Homo sapiens

<400> 209
Met Ala Ser Ala Leu Trp Thr Val Leu Pro Ser Arg Met Ser Leu
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Arg Ser Leu Lys Trp Ser Leu Leu Leu Leu Ser Leu Leu Ser Phe
20 25 30
Phe Val Met Trp Tyr Leu Ser Leu Pro His Tyr Asn Val Ile Glu
35 40 45
Arg Val Asn Trp Met Tyr Phe Tyr Glu Tyr Glu Pro Ile Tyr Arg
50 55 60
Gln Asp Phe His Phe Thr Leu Arg Glu His Ser Asn Cys Ser His
65 70 75
Gln Asn Pro Phe Leu Val Ile Leu Val Thr Ser His Pro Ser Asp
80 85 90
Val Lys Ala Arg Gln Ala Ile Arg Val Thr Trp Gly Glu Lys Lys
95 100 105
Ser Trp Trp Gly Tyr Glu Val Leu Thr Phe Phe Leu Leu Gly Gln
110 115 120
Glu Ala Glu Lys Glu Asp Lys Met Leu Ala Leu Ser Leu Glu Asp
125 130 135
Glu His Leu Leu Tyr Gly Asp Ile Ile Arg Gln Asp Phe Leu Asp
140 145 150
Thr Tyr Asn Asn Leu Thr Leu Lys Thr Ile Met Ala Phe Arg Trp
155 160 165

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aaaagt 1706

<210> 213
<211> 299
<212> PRT
<213> Homo sapiens

<400> 213

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Glu	Thr	Ile	Ala	Cys	Ala	Cys	Ile	Tyr	Leu	Ala	Ala	Arg	Ala	Leu	
				20					25					30	
Gln	Ile	Pro	Leu	Pro	Thr	Arg	Pro	His	Trp	Phe	Leu	Leu	Phe	Gly	
				35					40					45	
Thr	Thr	Glu	Glu	Glu	Ile	Gln	Glu	Ile	Cys	Ile	Glu	Thr	Leu	Arg	
				50					55					60	
Leu	Tyr	Thr	Arg	Lys	Lys	Pro	Asn	Tyr	Glu	Leu	Leu	Glu	Lys	Glu	
				65					70					75	
Val	Glu	Lys	Arg	Lys	Val	Ala	Leu	Gln	Glu	Ala	Lys	Leu	Lys	Ala	
				80					85					90	
Lys	Gly	Leu	Asn	Pro	Asp	Gly	Thr	Pro	Ala	Leu	Ser	Thr	Leu	Gly	
				95					100					105	
Gly	Phe	Ser	Pro	Ala	Ser	Lys	Pro	Ser	Ser	Pro	Arg	Glu	Val	Lys	
				110					115					120	
Ala	Glu	Glu	Lys	Ser	Pro	Ile	Ser	Ile	Asn	Val	Lys	Thr	Val	Lys	
				125					130					135	
Lys	Glu	Pro	Glu	Asp	Arg	Gln	Gln	Ala	Ser	Lys	Ser	Pro	Tyr	Asn	
				140					145					150	
Gly	Val	Arg	Lys	Asp	Ser	Lys	Arg	Ser	Arg	Asn	Ser	Arg	Ser	Ala	
				155					160					165	
Ser	Arg	Ser	Arg	Ser	Arg	Thr	Arg	Ser	Arg	Ser	Arg	Ser	His	Thr	
				170					175					180	
Pro	Arg	Arg	His	Tyr	Asn	Asn	Arg	Arg	Ser	Arg	Ser	Gly	Thr	Tyr	
				185					190					195	
Ser	Ser	Arg	Ser	Arg	Ser	Arg	Ser	Arg	Ser	His	Ser	Glu	Ser	Pro	
				200					205					210	
Arg	Arg	His	His	Asn	His	Gly	Ser	Pro	His	Leu	Lys	Ala	Lys	His	
				215					220					225	
Thr	Arg	Asp	Asp	Leu	Lys	Ser	Ser	Asn	Arg	His	Gly	His	Lys	Arg	
				230					235					240	
Lys	Lys	Ser	Arg	Ser	Arg	Ser	Gln	Ser	Lys	Ser	Arg	Asp	His	Ser	
				245					250					255	
Asp	Ala	Ala	Lys	Lys	His	Arg	His	Glu	Arg	Gly	His	His	Arg	Asp	
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04406660

285

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tcggggccctg gcggggaagc cgaggcccag aggcaggaaa gagcgggtggg 250
ccaatggcct tagtgaggag aagccactgt ctgtgccccg agatgccccg 300
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<210> 216

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Arg Pro His Leu Gln Ala Tyr Leu Cys	Leu Ala Lys Ala Arg Val	
335	340	345
Glu Gln Leu Arg Arg Glu Ala Gly Arg	Ile Glu Ala Arg Glu Ile	
350	355	360
Gln Gln Arg Val Val Arg Val Tyr Cys	Tyr Val Thr Val Val Ser	
365	370	375
Leu Gln Tyr Leu Thr Pro Leu Ile Leu	Thr Leu Asn Cys Thr Leu	
380	385	390
Leu Leu Lys Thr Leu Gly Gly Tyr Ser	Trp Gly Leu Gly Pro Ala	
395	400	405
Pro Leu Leu Ser Pro Asp Pro Ser Ser	Ala Ser Ala Ala Pro Ile	
410	415	420
Gly Ser Gly Glu Asp Glu Val Gln Gln	Thr Ala Ala Arg Ile Ala	
425	430	435
Gly Ala Leu Gly Gly Leu Leu Thr Pro	Leu Phe Leu Arg Gly Val	
440	445	450
Leu Ala Tyr Leu Ile Trp Trp Thr Ala	Ala Cys Gln Leu Leu Ala	
455	460	465
Ser Leu Phe Gly Leu Tyr Phe His Gln	His Leu Ala Gly Ser	
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<210> 217
 <211> 574
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 5, 146
 <223> unknown base

<400> 217
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 gctggctgct ctgtaacggc agtttggtcc gatacaagca cccgtnttga 150
 ggaggagctt cgggccctgg cggggaagcc gagggccaga ggcaggaaag 200
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ccagccaagg agactaacat tgctgtgttc tggcgcctgc tcacagtgc 450
cttctccatc aagatgttcc tgacagtgc acggtgtac ttcagcgccg 500
aggagggggg tgagcgctct gtctgcctca cctttgcctt cctcttcctg 550
ctgctggcca tgctggtgca agcg 574

<210> 218
<211> 2571
<212> DNA
<213> Homo sapiens

<400> 218
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ttgtgatcta ctgattgtgg gggcatggca aggtttgctt aaaggagctt 150
ggctgggttg ggcccttgta gctgacagaa ggtggccagg gagaatgcag 200
cacactgctc ggagaatgaa ggcgcttctg ttgctggtct tgccttggct 250
cagtctgct aactacattg acaatgtggg caacctgcac ttctgtatt 300
cagaactctg taaagggtgcc tccactacg gcctgaccaa agataggaag 350
aggcgctcac aagatggctg tccagacggc tgtgcgagcc tcacagccac 400
ggctccctcc ccagagggtt ctgcagctgc caccatctcc ttaatgacag 450
acgagcctgg cctagacaac cctgcctacg tgtcctcggc agaggacggg 500
cagccagcaa tcagcccagt ggactctggc cggagcaacc gaactagggc 550
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atcgagcttt gagtgttctt cgaaggacaa agagcgggag tgcagttgcc 650
aaccatgccg accagggcag ggaaaattct gaaaacacca ctgcccctga 700
agtctttcca aggttgtacc acctgattcc agatggtgaa attaccagca 750
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cccagatga cagctttcat gtgattctca acaaaagtag ccccgaggag 1100
cagcttgga taaaactggt gcgcaagggt gatgagcctg gggttttcat 1150
cttcaatgtg ctggatggcg gtgtggcata tcgacatggt cagcttgagg 1200

1	5	10	15
Asn Tyr Ile Asp	Asn Val Gly Asn Leu His	Phe Leu Tyr Ser	Glu
	20	25	30
Leu Cys Lys Gly	Ala Ser His Tyr Gly	Leu Thr Lys Asp Arg	Lys
	35	40	45
Arg Arg Ser Gln	Asp Gly Cys Pro Asp	Gly Cys Ala Ser Leu	Thr
	50	55	60
Ala Thr Ala Pro	Ser Pro Glu Val Ser	Ala Ala Thr Ile	Ser
	65	70	75
Leu Met Thr Asp	Glu Pro Gly Leu Asp	Asn Pro Ala Tyr Val	Ser
	80	85	90
Ser Ala Glu Asp	Gly Gln Pro Ala Ile	Ser Pro Val Asp Ser	Gly
	95	100	105
Arg Ser Asn Arg	Thr Arg Ala Arg Pro	Phe Glu Arg Ser Thr	Ile
	110	115	120
Arg Ser Arg Ser	Phe Lys Lys Ile Asn	Arg Ala Leu Ser Val	Leu
	125	130	135
Arg Arg Thr Lys	Ser Gly Ser Ala Val	Ala Asn His Ala Asp	Gln
	140	145	150
Gly Arg Glu Asn	Ser Glu Asn Thr Thr	Ala Pro Glu Val Phe	Pro
	155	160	165
Arg Leu Tyr His	Leu Ile Pro Asp Gly	Glu Ile Thr Ser Ile	Lys
	170	175	180
Ile Asn Arg Val	Asp Pro Ser Glu Ser	Leu Ser Ile Arg Leu	Val
	185	190	195
Gly Gly Ser Glu	Thr Pro Leu Val His	Ile Ile Ile Gln His	Ile
	200	205	210
Tyr Arg Asp Gly	Val Ile Ala Arg Asp	Gly Arg Leu Leu Pro	Gly
	215	220	225
Asp Ile Ile Leu	Lys Val Asn Gly Met	Asp Ile Ser Asn Val	Pro
	230	235	240
His Asn Tyr Ala	Val Arg Leu Leu Arg	Gln Pro Cys Gln Val	Leu
	245	250	255
Trp Leu Thr Val	Met Arg Glu Gln Lys	Phe Arg Ser Arg Asn	Asn
	260	265	270
Gly Gln Ala Pro	Asp Ala Tyr Arg Pro	Arg Asp Asp Ser Phe	His
	275	280	285
Val Ile Leu Asn	Lys Ser Ser Pro Glu	Glu Gln Leu Gly Ile	Lys
	290	295	300
Leu Val Arg Lys	Val Asp Glu Pro Gly	Val Phe Ile Phe Asn	Val
	305	310	315
Leu Asp Gly Gly	Val Ala Tyr Arg His	Gly Gln Leu Glu Glu	Asn

	320		325		330
Asp Arg Val Leu	Ala Ile Asn Gly His	Asp Leu Arg Tyr Gly Ser			
	335	340			345
Pro Glu Ser Ala	Ala His Leu Ile Gln	Ala Ser Glu Arg Arg Val			
	350	355			360
His Leu Val Val	Ser Arg Gln Val Arg	Gln Arg Ser Pro Asp Ile			
	365	370			375
Phe Gln Glu Ala	Gly Trp Asn Ser Asn	Gly Ser Trp Ser Pro Gly			
	380	385			390
Pro Gly Glu Arg	Ser Asn Thr Pro Lys	Pro Leu His Pro Thr Ile			
	395	400			405
Thr Cys His Glu	Lys Val Val Asn Ile	Gln Lys Asp Pro Gly Glu			
	410	415			420
Ser Leu Gly Met	Thr Val Ala Gly Gly	Ala Ser His Arg Glu Trp			
	425	430			435
Asp Leu Pro Ile	Tyr Val Ile Ser Val	Glu Pro Gly Gly Val Ile			
	440	445			450
Ser Arg Asp Gly	Arg Ile Lys Thr Gly	Asp Ile Leu Leu Asn Val			
	455	460			465
Asp Gly Val Glu	Leu Thr Glu Val Ser	Arg Ser Glu Ala Val Ala			
	470	475			480
Leu Leu Lys Arg	Thr Ser Ser Ser Ile	Val Leu Lys Ala Leu Glu			
	485	490			495
Val Lys Glu Tyr	Glu Pro Gln Glu Asp	Cys Ser Ser Pro Ala Ala			
	500	505			510
Leu Asp Ser Asn	His Asn Met Ala Pro	Pro Ser Asp Trp Ser Pro			
	515	520			525
Ser Trp Val Met	Trp Leu Glu Leu Pro	Arg Cys Leu Tyr Asn Cys			
	530	535			540
Lys Asp Ile Val	Leu Arg Arg Asn Thr	Ala Gly Ser Leu Gly Phe			
	545	550			555
Cys Ile Val Gly	Gly Tyr Glu Glu Tyr	Asn Gly Asn Lys Pro Phe			
	560	565			570
Phe Ile Lys Ser	Ile Val Glu Gly Thr	Pro Ala Tyr Asn Asp Gly			
	575	580			585
Arg Ile Arg Cys	Gly Asp Ile Leu Leu	Ala Val Asn Gly Arg Ser			
	590	595			600
Thr Ser Gly Met	Ile His Ala Cys Leu	Ala Arg Leu Leu Lys Glu			
	605	610			615
Leu Lys Gly Arg	Ile Thr Leu Thr Ile	Val Ser Trp Pro Gly Thr			
	620	625			630
Phe Leu					

<210> 220
 <211> 773
 <212> DNA
 <213> Homo sapiens

<400> 220
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 ccaggcaaat ggtgctgacc atctttggga tacaatctca tggatacgag 150
 gtttttaaca tcatcagccc aagcaacaat ggtggcaatg ttcaggagac 200
 agtgacaatt gataatgaaa aaaataccgc catcgttaac atccatgcag 250
 gatcatgctc ttctaccaca atttttgact ataaacatgg ctacattgca 300
 tccaggggtgc tctcccgaag agcctgcttt atcctgaaga tggaccatca 350
 gaacatccct cctctgaaca atctccaatg gtacatctat gagaaacagg 400
 ctctggacaa catgttctcc aacaaataca cctgggtcaa gtacaaccct 450
 ctggagtctc tgatcaaaga cgtggattgg ttctgtcttg ggtcaccat 500
 tgagaaactc tgcaaacata tccctttgta taagggggaa gtggttgaaa 550
 acacacataa tgtcggtgct ggaggctgtg caaaggctgg gctcctgggc 600
 atcttgggaa tttcaatctg tgcagacatt catgtttagg atgattagcc 650
 ctcttgtttt atcttttcaa agaaatacat ccttgggttta cactcaaaag 700
 tcaaattaaa ttctttccca atgcccacac taattttgag attcagtcag 750
 aaaatataaa tgctgtattt ata 773

<210> 221
 <211> 184
 <212> PRT
 <213> Homo sapiens

<400> 221
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 20 25 30
 Asn Asn Gly Gly Asn Val Gln Glu Thr Val Thr Ile Asp Asn Glu
 35 40 45
 Lys Asn Thr Ala Ile Val Asn Ile His Ala Gly Ser Cys Ser Ser
 50 55 60
 Thr Thr Ile Phe Asp Tyr Lys His Gly Tyr Ile Ala Ser Arg Val
 65 70 75
 Leu Ser Arg Arg Ala Cys Phe Ile Leu Lys Met Asp His Gln Asn
 80 85 90

Ile	Pro	Pro	Leu	Asn	Asn	Leu	Gln	Trp	Tyr	Ile	Tyr	Glu	Lys	Gln
				95					100					105
Ala	Leu	Asp	Asn	Met	Phe	Ser	Asn	Lys	Tyr	Thr	Trp	Val	Lys	Tyr
				110					115					120
Asn	Pro	Leu	Glu	Ser	Leu	Ile	Lys	Asp	Val	Asp	Trp	Phe	Leu	Leu
				125					130					135
Gly	Ser	Pro	Ile	Glu	Lys	Leu	Cys	Lys	His	Ile	Pro	Leu	Tyr	Lys
				140					145					150
Gly	Glu	Val	Val	Glu	Asn	Thr	His	Asn	Val	Gly	Ala	Gly	Gly	Cys
				155					160					165
Ala	Lys	Ala	Gly	Leu	Leu	Gly	Ile	Leu	Gly	Ile	Ser	Ile	Cys	Ala
				170					175					180

Asp Ile His Val

<210> 222
 <211> 992
 <212> DNA
 <213> Homo sapiens

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 tgccagcagc ttctccaagg cacgggagga agaaattacc cctgtggtct 150
 ccattgccta caaagtcctg gaagttttcc ccaaaggccg ctgggtgctc 200
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 tggaaccaag aacatcaagg tggccaagaa ggtggtgaag acccagcagc 300
 cggcctcctt caacctcaac gtcacactca agtccagtcc agacctgctc 350
 acctacttct gccgggcgtc ctccacctca ggtgcccagtg tggacagtgc 400
 caggctacag atgcactggg agctgtggtc caagccagtg tctgagctgc 450
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ggccatcagc gtgcactgtt cgtatttgga gttcatgcaa aatgagtgtg 950

ttttagctgc tcttgccaca aaaaaaaaaa aaaaaaaaaa aa 992

<210> 223

<211> 265

<212> PRT

<213> Homo sapiens

<400> 223

Met	Gly	Leu	Pro	Gly	Leu	Phe	Cys	Leu	Ala	Val	Leu	Ala	Ala	Ser	
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Ser	Phe	Ser	Lys	Ala	Arg	Glu	Glu	Glu	Ile	Thr	Pro	Val	Val	Ser	
				20					25					30	
Ile	Ala	Tyr	Lys	Val	Leu	Glu	Val	Phe	Pro	Lys	Gly	Arg	Trp	Val	
				35					40					45	
Leu	Ile	Thr	Cys	Cys	Ala	Pro	Gln	Pro	Pro	Pro	Pro	Ile	Thr	Tyr	
				50					55					60	
Ser	Leu	Cys	Gly	Thr	Lys	Asn	Ile	Lys	Val	Ala	Lys	Lys	Val	Val	
				65					70					75	
Lys	Thr	His	Glu	Pro	Ala	Ser	Phe	Asn	Leu	Asn	Val	Thr	Leu	Lys	
				80					85					90	
Ser	Ser	Pro	Asp	Leu	Leu	Thr	Tyr	Phe	Cys	Arg	Ala	Ser	Ser	Thr	
				95					100					105	
Ser	Gly	Ala	His	Val	Asp	Ser	Ala	Arg	Leu	Gln	Met	His	Trp	Glu	
				110					115					120	
Leu	Trp	Ser	Lys	Pro	Val	Ser	Glu	Leu	Arg	Ala	Asn	Phe	Thr	Leu	
				125					130					135	
Gln	Asp	Arg	Gly	Ala	Gly	Pro	Arg	Val	Glu	Met	Ile	Cys	Gln	Ala	
				140					145					150	
Ser	Ser	Gly	Ser	Pro	Pro	Ile	Thr	Asn	Ser	Leu	Ile	Gly	Lys	Asp	
				155					160					165	
Gly	Gln	Val	His	Leu	Gln	Gln	Arg	Pro	Cys	His	Arg	Gln	Pro	Ala	
				170					175					180	
Asn	Phe	Ser	Phe	Leu	Pro	Ser	Gln	Thr	Ser	Asp	Trp	Phe	Trp	Cys	
				185					190					195	
Gln	Ala	Ala	Asn	Asn	Ala	Asn	Val	Gln	His	Ser	Ala	Leu	Thr	Val	
				200					205					210	
Val	Pro	Pro	Gly	Gly	Asp	Gln	Lys	Met	Glu	Asp	Trp	Gln	Gly	Pro	
				215					220					225	
Leu	Glu	Ser	Pro	Ile	Leu	Ala	Leu	Pro	Leu	Tyr	Arg	Ser	Thr	Arg	
				230					235					240	
Arg	Leu	Ser	Glu	Glu	Glu	Phe	Gly	Gly	Phe	Arg	Ile	Gly	Asn	Gly	
				245					250					255	
Glu	Val	Arg	Gly	Arg	Lys	Ala	Ala	Ala	Met						
				260					265						

<210> 224
 <211> 1297
 <212> DNA
 <213> Homo sapiens

<400> 224
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 ggtggtgtgc ggttcaaggc caggtggatg aaaagacttt tcttcactat 200
 gactgtggca acaagacagt cacacctgtc agtcccctgg ggaagaaact 250
 aaatgtcaca acggcctgga aagcacagaa ccagtgactg agagagggtgg 300
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 cccaaggaac ccctcaccct gcaggcaagg atgtcttgtg agcagaaagc 400
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 gccagaaaga tgaaagaaaa gtgggagaat gacaaggttg tggccatgtc 550
 cttccattac ttctcaatgg gagactgtat aggatggctt gaggacttct 600
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 agcacggtct tgatcaaact cgcccttctg tctggccagc tgcccaogac 850
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 ccaatagctc attcactgcc ttgattcctt ttgccaacaa ttttaccagc 950
 agttatacct aacatattat gcaatcttct cttggtgcta cctgatggaa 1000
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 cttctctttt tgtttgaaa atcaagtact tctttgaatg atgatctctt 1100
 tcttgcaaat gatattgtca gtaaaataat cacgttagac ttcagacctc 1150
 tggggattct ttccgtgtcc tgaaagagaa tttttaaat atttaataag 1200
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<210> 225
 <211> 246
 <212> PRT
 <213> Homo sapiens

<400> 225

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Leu Leu Leu Leu Ser Gly Trp Ser Arg Ala Gly Arg Ala Asp Pro
          20           25           30

His Ser Leu Cys Tyr Asp Ile Thr Val Ile Pro Lys Phe Arg Pro
          35           40           45

Gly Pro Arg Trp Cys Ala Val Gln Gly Gln Val Asp Glu Lys Thr
          50           55           60

Phe Leu His Tyr Asp Cys Gly Asn Lys Thr Val Thr Pro Val Ser
          65           70           75

Pro Leu Gly Lys Lys Leu Asn Val Thr Thr Ala Trp Lys Ala Gln
          80           85           90

Asn Pro Val Leu Arg Glu Val Val Asp Ile Leu Thr Glu Gln Leu
          95           100          105

Arg Asp Ile Gln Leu Glu Asn Tyr Thr Pro Lys Glu Pro Leu Thr
          110          115          120

Leu Gln Ala Arg Met Ser Cys Glu Gln Lys Ala Glu Gly His Ser
          125          130          135

Ser Gly Ser Trp Gln Phe Ser Phe Asp Gly Gln Ile Phe Leu Leu
          140          145          150

Phe Asp Ser Glu Lys Arg Met Trp Thr Thr Val His Pro Gly Ala
          155          160          165

Arg Lys Met Lys Glu Lys Trp Glu Asn Asp Lys Val Val Ala Met
          170          175          180

Ser Phe His Tyr Phe Ser Met Gly Asp Cys Ile Gly Trp Leu Glu
          185          190          195

Asp Phe Leu Met Gly Met Asp Ser Thr Leu Glu Pro Ser Ala Gly
          200          205          210

Ala Pro Leu Ala Met Ser Ser Gly Thr Thr Gln Leu Arg Ala Thr
          215          220          225

Ala Thr Thr Leu Ile Leu Cys Cys Leu Leu Ile Ile Leu Pro Cys
          230          235          240

Phe Ile Leu Pro Gly Ile
          245

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<210> 226

<211> 735

<212> DNA

<213> Homo sapiens

<400> 226

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tgctgctagc tgccttgggc ctcacaattt tcattctggt ttctgacttt 100
caagttatat accgtggaat ggagttgatc ccaaccataa catcgtggag 150

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gcagaggatt ccaccttcaa aatcatgaac tctggctgtt gatcaaaaga 250
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ctgggccagg ctgtaatcag aattgtcgtc gtacatgctc aacagcattg 500
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ttacctttcc tctctccatt caagcattca aagtatatatt tcaatgaatt 600
aaaccttgca gcaagggacc ttagataggc ttattctgac tgtatgcttt 650
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gtattcattt tgaaaaaaaa aaaaaaaaaa aaaaa 735

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<211> 115
<212> PRT
<213> Homo sapiens

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Val Val Ala Leu Thr Gln Phe Trp Cys Gly Phe Leu Cys Arg Gly
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Phe His Leu Gln Asn His Glu Leu Trp Leu Leu Ile Lys Arg Glu
35 40 45
Phe Gly Phe Tyr Ser Lys Ser Gln Tyr Arg Thr Trp Gln Lys Lys
50 55 60
Leu Ala Glu Asp Ser Thr Trp Pro Pro Ile Asn Arg Thr Asp Tyr
65 70 75
Ser Gly Asp Gly Lys Asn Gly Phe Tyr Ile Asn Gly Gly Tyr Glu
80 85 90
Ser His Glu Gln Ile Pro Lys Arg Lys Leu Lys Leu Gly Gly Gln
95 100 105
Pro Thr Glu Gln His Phe Trp Ala Arg Leu
110 115

<210> 228
<211> 2185
<212> DNA
<213> Homo sapiens

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 gtttgctcgt gcagtaacca gttcagcaag gtggtgtgca cgcgccgggg 250
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 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Cys Pro Ser Val Cys Ser Cys Ser Asn Gln Phe Ser Lys Val Val
 50 55 60
 Cys Thr Arg Arg Gly Leu Ser Glu Val Pro Gln Gly Ile Pro Ser
 65 70 75
 Asn Thr Arg Tyr Leu Asn Leu Met Glu Asn Asn Ile Gln Met Ile
 80 85 90
 Gln Ala Asp Thr Phe Arg His Leu His His Leu Glu Val Leu Gln
 95 100 105
 Leu Gly Arg Asn Ser Ile Arg Gln Ile Glu Val Gly Ala Phe Asn
 110 115 120
 Gly Leu Ala Ser Leu Asn Thr Leu Glu Leu Phe Asp Asn Trp Leu
 125 130 135
 Thr Val Ile Pro Ser Gly Ala Phe Glu Tyr Leu Ser Lys Leu Arg
 140 145 150
 Glu Leu Trp Leu Arg Asn Asn Pro Ile Glu Ser Ile Pro Ser Tyr
 155 160 165
 Ala Phe Asn Arg Val Pro Ser Leu Met Arg Leu Asp Leu Gly Glu
 170 175 180
 Leu Lys Lys Leu Glu Tyr Ile Ser Glu Gly Ala Phe Glu Gly Leu

				185					190					195
Phe	Asn	Leu	Lys	Tyr 200	Leu	Asn	Leu	Gly	Met 205	Cys	Asn	Ile	Lys	Asp 210
Met	Pro	Asn	Leu	Thr 215	Pro	Leu	Val	Gly	Leu 220	Glu	Glu	Leu	Glu	Met 225
Ser	Gly	Asn	His	Phe 230	Pro	Glu	Ile	Arg	Pro 235	Gly	Ser	Phe	His	Gly 240
Leu	Ser	Ser	Leu	Lys 245	Lys	Leu	Trp	Val	Met 250	Asn	Ser	Gln	Val	Ser 255
Leu	Ile	Glu	Arg	Asn 260	Ala	Phe	Asp	Gly	Leu 265	Ala	Ser	Leu	Val	Glu 270
Leu	Asn	Leu	Ala	His 275	Asn	Asn	Leu	Ser	Ser 280	Leu	Pro	His	Asp	Leu 285
Phe	Thr	Pro	Leu	Arg 290	Tyr	Leu	Val	Glu	Leu 295	His	Leu	His	His	Asn 300
Pro	Trp	Asn	Cys	Asp 305	Cys	Asp	Ile	Leu	Trp 310	Leu	Ala	Trp	Trp	Leu 315
Arg	Glu	Tyr	Ile	Pro 320	Thr	Asn	Ser	Thr	Cys 325	Cys	Gly	Arg	Cys	His 330
Ala	Pro	Met	His	Met 335	Arg	Gly	Arg	Tyr	Leu 340	Val	Glu	Val	Asp	Gln 345
Ala	Ser	Phe	Gln	Cys 350	Ser	Ala	Pro	Phe	Ile 355	Met	Asp	Ala	Pro	Arg 360
Asp	Leu	Asn	Ile	Ser 365	Glu	Gly	Arg	Met	Ala 370	Glu	Leu	Lys	Cys	Arg 375
Thr	Pro	Pro	Met	Ser 380	Ser	Val	Lys	Trp	Leu 385	Leu	Pro	Asn	Gly	Thr 390
Val	Leu	Ser	His	Ala 395	Ser	Arg	His	Pro	Arg 400	Ile	Ser	Val	Leu	Asn 405
Asp	Gly	Thr	Leu	Asn 410	Phe	Ser	His	Val	Leu 415	Leu	Ser	Asp	Thr	Gly 420
Val	Tyr	Thr	Cys	Met 425	Val	Thr	Asn	Val	Ala 430	Gly	Asn	Ser	Asn	Ala 435
Ser	Ala	Tyr	Leu	Asn 440	Val	Ser	Thr	Ala	Glu 445	Leu	Asn	Thr	Ser	Asn 450
Tyr	Ser	Phe	Phe	Thr 455	Thr	Val	Thr	Val	Glu 460	Thr	Thr	Glu	Ile	Ser 465
Pro	Glu	Asp	Thr	Thr 470	Arg	Lys	Tyr	Lys	Pro 475	Val	Pro	Thr	Thr	Ser 480
Thr	Gly	Tyr	Gln	Pro 485	Ala	Tyr	Thr	Thr	Ser 490	Thr	Thr	Val	Leu	Ile 495
Gln	Thr	Thr	Arg	Val	Pro	Lys	Gln	Val	Ala	Val	Pro	Ala	Thr	Asp

500					505					510				
Thr	Thr	Asp	Lys	Met	Gln	Thr	Ser	Leu	Asp	Glu	Val	Met	Lys	Thr
				515					520					525
Thr	Lys	Ile	Ile	Ile	Gly	Cys	Phe	Val	Ala	Val	Thr	Leu	Leu	Ala
				530					535					540
Ala	Ala	Met	Leu	Ile	Val	Phe	Tyr	Lys	Leu	Arg	Lys	Arg	His	Gln
				545					550					555
Gln	Arg	Ser	Thr	Val	Thr	Ala	Ala	Arg	Thr	Val	Glu	Ile	Ile	Gln
				560					565					570
Val	Asp	Glu	Asp	Ile	Pro	Ala	Ala	Thr	Ser	Ala	Ala	Ala	Thr	Ala
				575					580					585
Ala	Pro	Ser	Gly	Val	Ser	Gly	Glu	Gly	Ala	Val	Val	Leu	Pro	Thr
				590					595					600
Ile	His	Asp	His	Ile	Asn	Tyr	Asn	Thr	Tyr	Lys	Pro	Ala	His	Gly
				605					610					615
Ala	His	Trp	Thr	Glu	Asn	Ser	Leu	Gly	Asn	Ser	Leu	His	Pro	Thr
				620					625					630
Val	Thr	Thr	Ile	Ser	Glu	Pro	Tyr	Ile	Ile	Gln	Thr	His	Thr	Lys
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Asp	Lys	Val	Gln	Glu	Thr	Gln	Ile							
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 <211> 2846
 <212> DNA
 <213> Homo sapiens

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 tacacagtca ttaatgaagc ctgccctgga gcagagtgga atatcatgtg 150
 tcgggagtgc tgtgaatatg atcagattga gtgcgtctgc cccggaaaga 200
 gggaagtctg gggttatacc atcccttgct gcaggaatga ggagaatgag 250
 tgtgactcct goctgatcca cccaggttgt accatctttg aaaactgcaa 300
 gagctgccga aatggctcat gggggggtac cttggatgac ttctatgtga 350
 aggggttcta ctgtgcagag tgccgagcag gctggtacgg aggagactgc 400
 atgcgatgtg gccaggttct gcgagcccca aagggtcaga ttttgttgga 450
 aagctatccc ctaaagtctc actgtgaatg gaccattcat gctaaacctg 500
 ggtttgtcat ccaactaaga tttgtcatgt tgagtctgga gtttgactac 550
 atgtgccagt atgactatgt tgaggttcgt gatggagaca accgcgatgg 600
 ccagatcatc aagcgtgtct gtggcaacga gcggccagct cctatccaga 650

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 cccttggtttc catgacggca cgtgcgtcct tgacaaggct ggatcttaca 800
 agtgtgcctg cttggcaggc tatactgggc agcgtgtga aaatctcctt 850
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<211> 720
<212> PRT
<213> Homo sapiens

<400> 231
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20 25 30
Glu Ala Cys Pro Gly Ala Glu Trp Asn Ile Met Cys Arg Glu Cys
35 40 45
Cys Glu Tyr Asp Gln Ile Glu Cys Val Cys Pro Gly Lys Arg Glu
50 55 60
Val Val Gly Tyr Thr Ile Pro Cys Cys Arg Asn Glu Glu Asn Glu
65 70 75
Cys Asp Ser Cys Leu Ile His Pro Gly Cys Thr Ile Phe Glu Asn
80 85 90
Cys Lys Ser Cys Arg Asn Gly Ser Trp Gly Gly Thr Leu Asp Asp
95 100 105
Phe Tyr Val Lys Gly Phe Tyr Cys Ala Glu Cys Arg Ala Gly Trp
110 115 120
Tyr Gly Gly Asp Cys Met Arg Cys Gly Gln Val Leu Arg Ala Pro
125 130 135
Lys Gly Gln Ile Leu Leu Glu Ser Tyr Pro Leu Asn Ala His Cys
140 145 150
Glu Trp Thr Ile His Ala Lys Pro Gly Phe Val Ile Gln Leu Arg
155 160 165

Phe	Val	Met	Leu	Ser	Leu	Glu	Phe	Asp	Tyr	Met	Cys	Gln	Tyr	Asp	
				170					175					180	
Tyr	Val	Glu	Val	Arg	Asp	Gly	Asp	Asn	Arg	Asp	Gly	Gln	Ile	Ile	
				185					190					195	
Lys	Arg	Val	Cys	Gly	Asn	Glu	Arg	Pro	Ala	Pro	Ile	Gln	Ser	Ile	
				200					205					210	
Gly	Ser	Ser	Leu	His	Val	Leu	Phe	His	Ser	Asp	Gly	Ser	Lys	Asn	
				215					220					225	
Phe	Asp	Gly	Phe	His	Ala	Ile	Tyr	Glu	Glu	Ile	Thr	Ala	Cys	Ser	
				230					235					240	
Ser	Ser	Pro	Cys	Phe	His	Asp	Gly	Thr	Cys	Val	Leu	Asp	Lys	Ala	
				245					250					255	
Gly	Ser	Tyr	Lys	Cys	Ala	Cys	Leu	Ala	Gly	Tyr	Thr	Gly	Gln	Arg	
				260					265					270	
Cys	Glu	Asn	Leu	Leu	Glu	Glu	Arg	Asn	Cys	Ser	Asp	Pro	Gly	Gly	
				275					280					285	
Pro	Val	Asn	Gly	Tyr	Gln	Lys	Ile	Thr	Gly	Gly	Pro	Gly	Leu	Ile	
				290					295					300	
Asn	Gly	Arg	His	Ala	Lys	Ile	Gly	Thr	Val	Val	Ser	Phe	Phe	Cys	
				305					310					315	
Asn	Asn	Ser	Tyr	Val	Leu	Ser	Gly	Asn	Glu	Lys	Arg	Thr	Cys	Gln	
				320					325					330	
Gln	Asn	Gly	Glu	Trp	Ser	Gly	Lys	Gln	Pro	Ile	Cys	Ile	Lys	Ala	
				335					340					345	
Cys	Arg	Glu	Pro	Lys	Ile	Ser	Asp	Leu	Val	Arg	Arg	Arg	Val	Leu	
				350					355					360	
Pro	Met	Gln	Val	Gln	Ser	Arg	Glu	Thr	Pro	Leu	His	Gln	Leu	Tyr	
				365					370					375	
Ser	Ala	Ala	Phe	Ser	Lys	Gln	Lys	Leu	Gln	Ser	Ala	Pro	Thr	Lys	
				380					385					390	
Lys	Pro	Ala	Leu	Pro	Phe	Gly	Asp	Leu	Pro	Met	Gly	Tyr	Gln	His	
				395					400					405	
Leu	His	Thr	Gln	Leu	Gln	Tyr	Glu	Cys	Ile	Ser	Pro	Phe	Tyr	Arg	
				410					415					420	
Arg	Leu	Gly	Ser	Ser	Arg	Arg	Thr	Cys	Leu	Arg	Thr	Gly	Lys	Trp	
				425					430					435	
Ser	Gly	Arg	Ala	Pro	Ser	Cys	Ile	Pro	Ile	Cys	Gly	Lys	Ile	Glu	
				440					445					450	
Asn	Ile	Thr	Ala	Pro	Lys	Thr	Gln	Gly	Leu	Arg	Trp	Pro	Trp	Gln	
				455					460					465	
Ala	Ala	Ile	Tyr	Arg	Arg	Thr	Ser	Gly	Val	His	Asp	Gly	Ser	Leu	
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<223> Synthetic oligonucleotide probe

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<210> 234
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 234
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<210> 235
<211> 1964
<212> DNA
<213> Homo sapiens

<400> 235
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caaattccga ttactgttgc tgttgacttt gtgcctgaca gtgggtgggt 200
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<210> 236

<211> 344

<212> PRT

<213> Homo sapiens

<220>

<221> Signal peptide

<222> 1-27

<223> Signal peptide

<220>

<221> N-glycosylation sites

<222> 4-7, 220-223, 335-338

<223> N-glycosylation sites

<220>

<221> Xylose isomerase proteins

<222> 191-201

<223> Xylose isomerase proteins

<400> 236

Met	Gly	Phe	Asn	Leu	Thr	Phe	His	Leu	Ser	Tyr	Lys	Phe	Arg	Leu
1					5				10					15

Leu	Leu	Leu	Leu	Thr	Leu	Cys	Leu	Thr	Val	Val	Gly	Trp	Ala	Thr	
				20					25					30	
Ser	Asn	Tyr	Phe	Val	Gly	Ala	Ile	Gln	Glu	Ile	Pro	Lys	Ala	Lys	
				35					40					45	
Glu	Phe	Met	Ala	Asn	Phe	His	Lys	Thr	Leu	Ile	Leu	Gly	Lys	Gly	
				50					55					60	
Lys	Thr	Leu	Thr	Asn	Glu	Ala	Ser	Thr	Lys	Lys	Val	Glu	Leu	Asp	
				65					70					75	
Asn	Cys	Pro	Ser	Val	Ser	Pro	Tyr	Leu	Arg	Gly	Gln	Ser	Lys	Leu	
				80					85					90	
Ile	Phe	Lys	Pro	Asp	Leu	Thr	Leu	Glu	Glu	Val	Gln	Ala	Glu	Asn	
				95					100					105	
Pro	Lys	Val	Ser	Arg	Gly	Arg	Tyr	Arg	Pro	Gln	Glu	Cys	Lys	Ala	
				110					115					120	
Leu	Gln	Arg	Val	Ala	Ile	Leu	Val	Pro	His	Arg	Asn	Arg	Glu	Lys	
				125					130					135	
His	Leu	Met	Tyr	Leu	Leu	Glu	His	Leu	His	Pro	Phe	Leu	Gln	Arg	
				140					145					150	
Gln	Gln	Leu	Asp	Tyr	Gly	Ile	Tyr	Val	Ile	His	Gln	Ala	Glu	Gly	
				155					160					165	
Lys	Lys	Phe	Asn	Arg	Ala	Lys	Leu	Leu	Asn	Val	Gly	Tyr	Leu	Glu	
				170					175					180	
Ala	Leu	Lys	Glu	Glu	Asn	Trp	Asp	Cys	Phe	Ile	Phe	His	Asp	Val	
				185					190					195	
Asp	Leu	Val	Pro	Glu	Asn	Asp	Phe	Asn	Leu	Tyr	Lys	Cys	Glu	Glu	
				200					205					210	
His	Pro	Lys	His	Leu	Val	Val	Gly	Arg	Asn	Ser	Thr	Gly	Tyr	Arg	
				215					220					225	
Leu	Arg	Tyr	Ser	Gly	Tyr	Phe	Gly	Gly	Val	Thr	Ala	Leu	Ser	Arg	
				230					235					240	
Glu	Gln	Phe	Phe	Lys	Val	Asn	Gly	Phe	Ser	Asn	Asn	Tyr	Trp	Gly	
				245					250					255	
Trp	Gly	Gly	Glu	Asp	Asp	Asp	Leu	Arg	Leu	Arg	Val	Glu	Leu	Gln	
				260					265					270	
Arg	Met	Lys	Ile	Ser	Arg	Pro	Leu	Pro	Glu	Val	Gly	Lys	Tyr	Thr	
				275					280					285	
Met	Val	Phe	His	Thr	Arg	Asp	Lys	Gly	Asn	Glu	Val	Asn	Ala	Glu	
				290					295					300	
Arg	Met	Lys	Leu	Leu	His	Gln	Val	Ser	Arg	Val	Trp	Arg	Thr	Asp	
				305					310					315	
Gly	Leu	Ser	Ser	Cys	Ser	Tyr	Lys	Leu	Val	Ser	Val	Glu	His	Asn	
				320					325					330	

Pro Leu Tyr Ile Asn Ile Thr Val Asp Phe Trp Phe Gly Ala
 335 340

<210> 237
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 237
 ccttacctca gaggccagag caagc 25

<210> 238
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 238
 gagcttcac tcgttctgcgt tcacc 25

<210> 239
 <211> 46
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 239
 caggaatgta aagctttaca gagggctcgcc atcctcggtc cccacc 46

<210> 240
 <211> 2567
 <212> DNA
 <213> Homo sapiens

<400> 240
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 gccgcagttc tcgagctcca gctgcattcc ctccgcgtcc gcccacgct 100
 tctcccgtc cgggccccgc aatggcccag gcagtgtggt cgcgcctcgg 150
 ccgcatactc tggtttgcct gcctcctgcc ctgggccccg gcaggggtgg 200
 ccgcaggcct gtatgaactc aatctcacca ccgatagccc tgccaccacg 250
 ggagcgggtg tgaccatctc ggccagcctg gtggccaagg acaacggcag 300
 cctggccctg cccgctgacg cccacctcta ccgcttcac tggatccaca 350
 ccccgctggt gcttactggc aagatggaga aggtctcag ctccaccatc 400
 cgtgtggtcg gccacgtgcc cggggaattc ccggtctctg tctgggtcac 450
 tgccgctgac tgctggatgt gccagcctgt ggccaggggc tttgtgtcc 500
 tccccatcac agagttcctc gtgggggacc ttgttgcac ccagaacact 550

tccctaccct ggcccagctc ctatctcact aagaccgtcc tgaaagtctc 600
 cticctcctc cagcaccga gcaacttcct caagaccgcc ttgtttctct 650
 acagctggga cttcggggac gggaccaga tggtgactga agactccgtg 700
 gtctattata actattccat catcgggacc ttcaccgtga agotcaaagt 750
 ggtggcgag tgggaagagg tggagccgga tgccacgagg gctgtgaagc 800
 agaagaccgg ggactttctc gcctcgtga agctgcagga aacccttcga 850
 ggcatccaag tgttggggcc caccctaatt cagaccttc aaaagatgac 900
 cgtgacctg aacttcctgg ggagccctc tctgactgtg tgctggcgtc 950
 tcaagcctga gtgcctcccg ctggaggaag gggagtgcc ccctgtgtcc 1000
 gtggccagca cagcgtacaa cctgaccac accttcaggg accctgggga 1050
 ctactgcttc agcatccggg ccgagaatat catcagcaag acacatcagt 1100
 accacaagat ccaggtgtgg ccctccagaa tccagccggc tgtctttgct 1150
 ttcccatgtg ctacacttat cactgtgatg ttggccttca tcatgtacat 1200
 gaccctgcgg aatgccactc agcaaaagga catggtggag aaccgggagc 1250
 caccctctgg ggtcaggtgc tgctgccaga tgtgctgtgg gcctttcttg 1300
 ctggagactc catctgagta cctggaaatt gttcgtgaga accacgggct 1350
 gctcccgccc ctctataagt ctgtcaaac ttacaccgtg tgagcactcc 1400
 ccctcccccac cccatctcag tgttaactga ctgctgactt ggagtttcca 1450
 gcagggtggt gtgcaccact gaccaggagg ggttcatttg cgtggggctg 1500
 ttggcctgga tcatccatcc atctgtacag ttcagccact gccacaagcc 1550
 cctccctctc tgtcaccct gacccagcc attcaccat ctgtacagtc 1600
 cagccactga cataagcccc actcggttac cacccttg acccctacc 1650
 tttgaagagg cttcgtgcag gactttgatg cttggggtgt tccgtgttga 1700
 ctctaggtg ggctggctg cccactgcc attcctctca tattggcaca 1750
 tctgctgtcc attgggggtt ctgagtttc tccccagac agccctacct 1800
 gtgccagaga gctagaaaga aggtcataaa gggtaaaaa tccataacta 1850
 aaggttgtac acatagatgg gcacactcac agagagaagt gtgcatgtac 1900
 acacaccaca cacacacaca cacacacaca cacagaaata taaacacatg 1950
 cgtcacatgg gcatttcaga tgatcagctc tgtatctggt taagtcggtt 2000
 gctgggatgc accctgcact agagctgaaa ggaaatttga cctccaagca 2050
 gcctgacag gttctgggcc cgggccctcc ctttgtgctt tgtctctgca 2100
 gttcttgcc cctttataag gccatcctag tccctgctgg ctggcagggg 2150

cctggatggg gggcaggact aatactgagt gattgcagag tgctttataa 2200
 atatcacctt attttatcga aacccatctg tgaaactttc actgaggaaa 2250
 aggccttgca gcggtagaag aggttgagtc aaggccgggc gcggtggctc 2300
 acgcctgtaa tcccagcact ttgggaggcc gaggcgggtg gatcacgaga 2350
 tcaggagatc gagaccacc tggctaacac ggtgaaaccc cgtctctact 2400
 aaaaaatac aaaaagttag ccgggcgtgg tgggtgggtgc ctgtagtccc 2450
 agctactcgg gaggctgagg caggagaatg gtgcgaaccc gggaggcgga 2500
 gcttgcatg agcccagatg gcgccactgc actccagcct gagtgacaga 2550
 gcgagactct gtctcca 2567

<210> 241
 <211> 423
 <212> PRT
 <213> Homo sapiens

<400> 241
 Met Ala Gln Ala Val Trp Ser Arg Leu Gly Arg Ile Leu Trp Leu
 1 5 10 15
 Ala Cys Leu Leu Pro Trp Ala Pro Ala Gly Val Ala Ala Gly Leu
 20 25 30
 Tyr Glu Leu Asn Leu Thr Thr Asp Ser Pro Ala Thr Thr Gly Ala
 35 40 45
 Val Val Thr Ile Ser Ala Ser Leu Val Ala Lys Asp Asn Gly Ser
 50 55 60
 Leu Ala Leu Pro Ala Asp Ala His Leu Tyr Arg Phe His Trp Ile
 65 70 75
 His Thr Pro Leu Val Leu Thr Gly Lys Met Glu Lys Gly Leu Ser
 80 85 90
 Ser Thr Ile Arg Val Val Gly His Val Pro Gly Glu Phe Pro Val
 95 100 105
 Ser Val Trp Val Thr Ala Ala Asp Cys Trp Met Cys Gln Pro Val
 110 115 120
 Ala Arg Gly Phe Val Val Leu Pro Ile Thr Glu Phe Leu Val Gly
 125 130 135
 Asp Leu Val Val Thr Gln Asn Thr Ser Leu Pro Trp Pro Ser Ser
 140 145 150
 Tyr Leu Thr Lys Thr Val Leu Lys Val Ser Phe Leu Leu His Asp
 155 160 165
 Pro Ser Asn Phe Leu Lys Thr Ala Leu Phe Leu Tyr Ser Trp Asp
 170 175 180
 Phe Gly Asp Gly Thr Gln Met Val Thr Glu Asp Ser Val Val Tyr
 185 190 195

Tyr	Asn	Tyr	Ser	Ile	Ile	Gly	Thr	Phe	Thr	Val	Lys	Leu	Lys	Val
				200					205					210
Val	Ala	Glu	Trp	Glu	Glu	Val	Glu	Pro	Asp	Ala	Thr	Arg	Ala	Val
				215					220					225
Lys	Gln	Lys	Thr	Gly	Asp	Phe	Ser	Ala	Ser	Leu	Lys	Leu	Gln	Glu
				230					235					240
Thr	Leu	Arg	Gly	Ile	Gln	Val	Leu	Gly	Pro	Thr	Leu	Ile	Gln	Thr
				245					250					255
Phe	Gln	Lys	Met	Thr	Val	Thr	Leu	Asn	Phe	Leu	Gly	Ser	Pro	Pro
				260					265					270
Leu	Thr	Val	Cys	Trp	Arg	Leu	Lys	Pro	Glu	Cys	Leu	Pro	Leu	Glu
				275					280					285
Glu	Gly	Glu	Cys	His	Pro	Val	Ser	Val	Ala	Ser	Thr	Ala	Tyr	Asn
				290					295					300
Leu	Thr	His	Thr	Phe	Arg	Asp	Pro	Gly	Asp	Tyr	Cys	Phe	Ser	Ile
				305					310					315
Arg	Ala	Glu	Asn	Ile	Ile	Ser	Lys	Thr	His	Gln	Tyr	His	Lys	Ile
				320					325					330
Gln	Val	Trp	Pro	Ser	Arg	Ile	Gln	Pro	Ala	Val	Phe	Ala	Phe	Pro
				335					340					345
Cys	Ala	Thr	Leu	Ile	Thr	Val	Met	Leu	Ala	Phe	Ile	Met	Tyr	Met
				350					355					360
Thr	Leu	Arg	Asn	Ala	Thr	Gln	Gln	Lys	Asp	Met	Val	Glu	Asn	Pro
				365					370					375
Glu	Pro	Pro	Ser	Gly	Val	Arg	Cys	Cys	Cys	Gln	Met	Cys	Cys	Gly
				380					385					390
Pro	Phe	Leu	Leu	Glu	Thr	Pro	Ser	Glu	Tyr	Leu	Glu	Ile	Val	Arg
				395					400					405
Glu	Asn	His	Gly	Leu	Leu	Pro	Pro	Leu	Tyr	Lys	Ser	Val	Lys	Thr
				410					415					420

Tyr Thr Val

- <210> 242
- <211> 26
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> Synthetic oligonucleotide probe
- <400> 242
- catttcctta ccctggaccc agctcc 26
- <210> 243
- <211> 25
- <212> DNA
- <213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 243
gaaaggccca cagcacatct ggcag 25

<210> 244
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 244
ccacgaccg agcaacttcc tcaagaccga cttgtttctc tacagc 46

<210> 245
<211> 485
<212> DNA
<213> Homo sapiens

<400> 245
gctcaagacc cagcagtggg acagccagac agacggcacg atggcactga 50
gctcccagat ctgggccgct tgcctcctgc tctcctcct cctcgccagc 100
ctgaccagtg gctctgtttt cccacaacag acgggacaac ttgcagagct 150
gcaaccccg gacagagctg gagccagggc cagctggatg cccatgttcc 200
agaggcgaag gaggcgagac acccacttcc ccatctgcat tttctgctgc 250
ggctgctgtc atcgatcaaa gtgtgggatg tgctgcaaga cgtagaacct 300
acctgccctg ccccgctccc ctcccttcct tatttattcc tgctgcccc 350
gaacataggt cttggaataa aatggctggt tcttttgttt tccaaaaaaaa 400
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 450
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 485

<210> 246
<211> 84
<212> PRT
<213> Homo sapiens

<400> 246
Met Ala Leu Ser Ser Gln Ile Trp Ala Ala Cys Leu Leu Leu Leu
1 5 10 15
Leu Leu Leu Ala Ser Leu Thr Ser Gly Ser Val Phe Pro Gln Gln
20 25 30
Thr Gly Gln Leu Ala Glu Leu Gln Pro Gln Asp Arg Ala Gly Ala
35 40 45
Arg Ala Ser Trp Met Pro Met Phe Gln Arg Arg Arg Arg Arg Asp
50 55 60
Thr His Phe Pro Ile Cys Ile Phe Cys Cys Gly Cys Cys His Arg
65 70 75

Ser Lys Cys Gly Met Cys Cys Lys Thr
80

<210> 247
<211> 2359
<212> DNA
<213> Homo sapiens

<400> 247
ctgtcaggaa ggaccatctg aaggctgcaa tttgtttotta gggagggcagg 50
tgctggcctg gcctggatct tccaccatgt tctgtttgct gccttttgat 100
agcctgattg tcaaccttct gggcatctcc ctgactgtcc tcttcaccct 150
ccttctcgtt ttcattcatag tgccagccat ttttggagtc tcctttggta 200
tccgcaaact ctacatgaaa agtctgttaa aaatctttgc gtgggctacc 250
ttgagaatgg agcgaggagc caaggagaag aaccaccagc tttacaagcc 300
ctacaccaac ggaatcattg caaaggatcc cacttcaacta gaagaagaga 350
tcaaagagat tcgtcgaagt ggtagtagta aggctctgga caaactcca 400
gagttcgagc tctctgacat tttctacttt tgccggaaag gaatggagac 450
cattatggat gatgaggatg caaagagatt ctgagcagaa gaactggagt 500
cctggaacct gctgagcaga accaattata acttccagta catcagcctt 550
cggctcacgg tcctgtgggg gttaggagtg ctgattcggc actgctttct 600
gctgocgctc aggatagcac tggctttcac agggattagc cttctgggtg 650
tgggcacaaac tgtggtggga tacttgccaa atgggaggtt taagggaattc 700
atgagtaaac atgttcactt aatgtgttac cggatctgag tgcgagcgc 750
gacagccatc atcaoctacc atgacagga aaacagacca agaaatggtg 800
gcatctgtgt ggccaatcat acctcaccga tcgatgtgat catcttggcc 850
agcgatggct attatgccat ggtgggtcaa gtgcacgggg gactcatggg 900
tgtgattcag agagccatgg tgaaggcctg cccacacgctc tggtttgagc 950
gctcggaagt gaaggatcgc cacctggtgg ctaagagact gactgaacat 1000
gtgcaagata aaagcaagct gcctatcctc atcttcccag aaggaacctg 1050
catcaataat acatcgggtg tgatgttcaa aaagggaagt tttgaaattg 1100
gagccacagt ttacctgtt gctatcaagt atgaccctca atttgcgat 1150
gccttctgga acagcagcaa atacgggatg gtgacgtacc tgctgcgaat 1200
gatgaccagc tgggccattg tctgcagcgt gtggtacctg cctcccatga 1250
ctagagaggc agatgaagat gctgtccagt ttgcgaatag ggtgaaatct 1300
gccattgcca ggcagggagg acttgtggac ctgctgtggg atgggggcct 1350

gaagagggag aaggtgaagg acacgttcaa ggaggagcag cagaagctgt 1400
acagcaagat gatcgtgggg aaccacaagg acaggagccg ctcttgagcc 1450
tgcctccagc tggctggggc caccgtgcgg ggtgccaacg ggctcagagc 1500
tggagttgcc gccgccgccc ccaactgctgt gtcctttcca gactccaggg 1550
ctccccgggc tgctctggat cccaggactc cggctttcgc cgagccgcag 1600
cgggatccct gtgcacccgg cgcagcctac ccttggtggt ctaaaccgat 1650
gctgctgggt gttgcgaccc aggacgagat gccttgtttc ttttacaata 1700
agtcgttgga ggaatgccat taaagtgaac tccccacctt tgcacgctgt 1750
gcgggctgag tggttgggga gatgtggcca tggctctgtg ctagagatgg 1800
cggtaacaaga gtctgttatg caagcccgtg tgccagggat gtgctggggg 1850
cggccacccg ctctccagga aaggcacagc tgaggcactg tggctggcctt 1900
cggcctcaac atcgccccca gccttgagc tctgcagaca tgataggaag 1950
gaaactgtca tctgcagggg ctttcagcaa aatgaagggt tagattttta 2000
tgctgctgct gatgggggta ctaaaggag gggaaggagc cagggtgggcc 2050
gctgactggg ccatggggag aacgtgtgtt cgtactccag gctaaccctg 2100
aactccccat gtgatgcgcg ctttggtgaa tgtgtgtctc ggtttcccca 2150
tctgtaatat gagtcggggg gaatggtggt gattcctacc tcacagggct 2200
gttggtgggga ttaaagtgtc gcgggtgagt gaaggacaca tcacgttcag 2250
tgtttcaagt acaggcccac aaaacggggc acggcaggcc tgagctcaga 2300
gctgctgcac tgggctttgg atttgttctt gtgagtaaata aaaactggct 2350
ggtgaatga 2359

<210> 248

<211> 456

<212> PRT

<213> Homo sapiens

<400> 248

Met	Phe	Leu	Leu	Leu	Pro	Phe	Asp	Ser	Leu	Ile	Val	Asn	Leu	Leu
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Gly	Ile	Ser	Leu	Thr	Val	Leu	Phe	Thr	Leu	Leu	Leu	Val	Phe	Ile
				20					25					30
Ile	Val	Pro	Ala	Ile	Phe	Gly	Val	Ser	Phe	Gly	Ile	Arg	Lys	Leu
				35					40					45
Tyr	Met	Lys	Ser	Leu	Leu	Lys	Ile	Phe	Ala	Trp	Ala	Thr	Leu	Arg
				50					55					60
Met	Glu	Arg	Gly	Ala	Lys	Glu	Lys	Asn	His	Gln	Leu	Tyr	Lys	Pro
				65					70					75

Tyr	Thr	Asn	Gly	Ile	Ile	Ala	Lys	Asp	Pro	Thr	Ser	Leu	Glu	Glu	
				80					85					90	
Glu	Ile	Lys	Glu	Ile	Arg	Arg	Ser	Gly	Ser	Ser	Lys	Ala	Leu	Asp	
				95					100					105	
Asn	Thr	Pro	Glu	Phe	Glu	Leu	Ser	Asp	Ile	Phe	Tyr	Phe	Cys	Arg	
				110					115					120	
Lys	Gly	Met	Glu	Thr	Ile	Met	Asp	Asp	Glu	Val	Thr	Lys	Arg	Phe	
				125					130					135	
Ser	Ala	Glu	Glu	Leu	Glu	Ser	Trp	Asn	Leu	Leu	Ser	Arg	Thr	Asn	
				140					145					150	
Tyr	Asn	Phe	Gln	Tyr	Ile	Ser	Leu	Arg	Leu	Thr	Val	Leu	Trp	Gly	
				155					160					165	
Leu	Gly	Val	Leu	Ile	Arg	Tyr	Cys	Phe	Leu	Leu	Pro	Leu	Arg	Ile	
				170					175					180	
Ala	Leu	Ala	Phe	Thr	Gly	Ile	Ser	Leu	Leu	Val	Val	Gly	Thr	Thr	
				185					190					195	
Val	Val	Gly	Tyr	Leu	Pro	Asn	Gly	Arg	Phe	Lys	Glu	Phe	Met	Ser	
				200					205					210	
Lys	His	Val	His	Leu	Met	Cys	Tyr	Arg	Ile	Cys	Val	Arg	Ala	Leu	
				215					220					225	
Thr	Ala	Ile	Ile	Thr	Tyr	His	Asp	Arg	Glu	Asn	Arg	Pro	Arg	Asn	
				230					235					240	
Gly	Gly	Ile	Cys	Val	Ala	Asn	His	Thr	Ser	Pro	Ile	Asp	Val	Ile	
				245					250					255	
Ile	Leu	Ala	Ser	Asp	Gly	Tyr	Tyr	Ala	Met	Val	Gly	Gln	Val	His	
				260					265					270	
Gly	Gly	Leu	Met	Gly	Val	Ile	Gln	Arg	Ala	Met	Val	Lys	Ala	Cys	
				275					280					285	
Pro	His	Val	Trp	Phe	Glu	Arg	Ser	Glu	Val	Lys	Asp	Arg	His	Leu	
				290					295					300	
Val	Ala	Lys	Arg	Leu	Thr	Glu	His	Val	Gln	Asp	Lys	Ser	Lys	Leu	
				305					310					315	
Pro	Ile	Leu	Ile	Phe	Pro	Glu	Gly	Thr	Cys	Ile	Asn	Asn	Thr	Ser	
				320					325					330	
Val	Met	Met	Phe	Lys	Lys	Gly	Ser	Phe	Glu	Ile	Gly	Ala	Thr	Val	
				335					340					345	
Tyr	Pro	Val	Ala	Ile	Lys	Tyr	Asp	Pro	Gln	Phe	Gly	Asp	Ala	Phe	
				350					355					360	
Trp	Asn	Ser	Ser	Lys	Tyr	Gly	Met	Val	Thr	Tyr	Leu	Leu	Arg	Met	
				365					370					375	
Met	Thr	Ser	Trp	Ala	Ile	Val	Cys	Ser	Val	Trp	Tyr	Leu	Pro	Pro	
				380					385					390	

Met	Thr	Arg	Glu	Ala	Asp	Glu	Asp	Ala	Val	Gln	Phe	Ala	Asn	Arg
				395					400					405
Val	Lys	Ser	Ala	Ile	Ala	Arg	Gln	Gly	Gly	Leu	Val	Asp	Leu	Leu
				410					415					420
Trp	Asp	Gly	Gly	Leu	Lys	Arg	Glu	Lys	Val	Lys	Asp	Thr	Phe	Lys
				425					430					435
Glu	Glu	Gln	Gln	Lys	Leu	Tyr	Ser	Lys	Met	Ile	Val	Gly	Asn	His
				440					445					450
Lys	Asp	Arg	Ser	Arg	Ser									
				455										

<210> 249
 <211> 1103
 <212> DNA
 <213> Homo sapiens

<400> 249
 gccctcgaa accaggactc cagcacctct ggtcccgccc tcacccggac 50
 ccctggccct cactgtctct ccagggatgg cgctggcggc tttgatgatc 100
 gccctcgga gcttcggcct ccacacctgg caggcccagg ctgttccac 150
 catcctgccc ctgggcctgg ctccagacac ctttgacgat acctatgtgg 200
 gttgtgcaga ggagatggag gagaaggcag cccccctgct aaaggaggaa 250
 atggcccacc atgccctgct gcgggaatcc tgggaggcag cccaggagac 300
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 tgggagttga atcaggccgt gcggacgggc ggaggctccc gggagctcta 450
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<211> 240

<212> PRT

<213> Homo sapiens

<400> 250

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20 25 30

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35 40 45

Glu Met Glu Glu Lys Ala Ala Pro Leu Leu Lys Glu Glu Met Ala
50 55 60

His His Ala Leu Leu Arg Glu Ser Trp Glu Ala Ala Gln Glu Thr
65 70 75

Trp Glu Asp Lys Arg Arg Gly Leu Thr Leu Pro Pro Gly Phe Lys
80 85 90

Ala Gln Asn Gly Ile Ala Ile Met Val Tyr Thr Asn Ser Ser Asn
95 100 105

Thr Leu Tyr Trp Glu Leu Asn Gln Ala Val Arg Thr Gly Gly Gly
110 115 120

Ser Arg Glu Leu Tyr Met Arg His Phe Pro Phe Lys Ala Leu His
125 130 135

Phe Tyr Leu Ile Arg Ala Leu Gln Leu Leu Arg Gly Ser Gly Gly
140 145 150

Cys Ser Arg Gly Pro Gly Glu Val Val Phe Arg Gly Val Gly Ser
155 160 165

Leu Arg Phe Glu Pro Lys Arg Leu Gly Asp Ser Val Arg Leu Gly
170 175 180

Gln Phe Ala Ser Ser Ser Leu Asp Lys Ala Val Ala His Arg Phe
185 190 195

Gly Glu Lys Arg Arg Gly Cys Val Ser Ala Pro Gly Val Gln Leu
200 205 210

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<210> 251

<211> 50

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

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<210> 252
<211> 1076
<212> DNA
<213> Homo sapiens

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tggggatata cagctcatca ctccagcagc cctccacca ggagtacgtg 400
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tcacactaat agaacaatcc taaaggaaga tccagcaaat acggtttact 950
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<210> 253
<211> 335
<212> PRT
<213> Homo sapiens

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Gly Ser Val Gly Gly	Ala Val Thr Phe	Pro Leu Lys Ser Lys Val	35 40 45
Lys Gln Val Asp Ser	Ile Val Trp Thr	Phe Asn Thr Thr Pro Leu	50 55 60
Val Thr Ile Gln Pro	Glu Gly Gly Thr	Ile Ile Val Thr Gln Asn	65 70 75
Arg Asn Arg Glu Arg	Val Asp Phe Pro	Asp Gly Gly Tyr Ser Leu	80 85 90
Lys Leu Ser Lys Leu	Lys Lys Asn Asp	Ser Gly Ile Tyr Tyr Val	95 100 105
Gly Ile Tyr Ser Ser	Ser Leu Gln Gln	Pro Ser Thr Gln Glu Tyr	110 115 120
Val Leu His Val Tyr	Glu His Leu Ser	Lys Pro Lys Val Thr Met	125 130 135
Gly Leu Gln Ser Asn	Lys Asn Gly Thr	Cys Val Thr Asn Leu Thr	140 145 150
Cys Cys Met Glu His	Gly Glu Glu Asp	Val Ile Tyr Thr Trp Lys	155 160 165
Ala Leu Gly Gln Ala	Ala Asn Glu Ser	His Asn Gly Ser Ile Leu	170 175 180
Pro Ile Ser Trp Arg	Trp Gly Glu Ser	Asp Met Thr Phe Ile Cys	185 190 195
Val Ala Arg Asn Pro	Val Ser Arg Asn	Phe Ser Ser Pro Ile Leu	200 205 210
Ala Arg Lys Leu Cys	Glu Gly Ala Ala	Asp Asp Pro Asp Ser Ser	215 220 225
Met Val Leu Leu Cys	Leu Leu Leu Val	Pro Leu Leu Leu Ser Leu	230 235 240
Phe Val Leu Gly Leu	Phe Leu Trp Phe	Leu Lys Arg Glu Arg Gln	245 250 255
Glu Glu Tyr Ile Glu	Glu Lys Lys Arg	Val Asp Ile Cys Arg Glu	260 265 270
Thr Pro Asn Ile Cys	Pro His Ser Gly	Glu Asn Thr Glu Tyr Asp	275 280 285
Thr Ile Pro His Thr	Asn Arg Thr Ile	Leu Lys Glu Asp Pro Ala	290 295 300
Asn Thr Val Tyr Ser	Thr Val Glu Ile	Pro Lys Lys Met Glu Asn	305 310 315
Pro His Ser Leu Leu	Thr Met Pro Asp	Thr Pro Arg Leu Phe Ala	

330

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<211> 1053
<212> DNA
<213> Homo sapiens
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<211> 860
<212> DNA
<213> Homo sapiens
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226

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Gly	Leu	Tyr	Gly	Arg	Glu	Pro	Asp	Leu	Ser	Ser	Asp	Ile	Lys	Glu
				140					145					150
Arg	Phe	Ala	Gln	Leu	Cys	Glu	Glu	His	Gly	Ile	Leu	Arg	Glu	Asn
				155					160					165
Ile	Ile	Asp	Leu	Ser	Asn	Ala	Asn	Arg	Cys	Leu	Gln	Ala	Arg	Glu
				170					175					180

<210> 257
 <211> 766
 <212> DNA
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 ttctcaatgc gatacctcta attgtcagct tagttgagga agaccaattt 150
 tctcaaaacc ccatctcttg ctttgagtgg tggttcccag gaattatagg 200
 agcaggtctg atggccattc cagcaacaac aatgtccttg acagcaagaa 250
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 agtgtgatca cagtcattgg tgctctgtat tgcattgctga tatccatcca 350
 ggctctctta aaaggtcctc tcatgtgtaa ttctccaagc aacagtaatg 400
 ccaattgtga attttcattg aaaaacatca gtgacattca tccagaatcc 450
 ttcaacttgc agtggttttt caatgactct tgtgcacctc ctactggttt 500
 caataaacc accagtaacg acaccatggc gagggtgctg agagcatcta 550
 gtttccactt cgattctgaa gaaaacaaac ataggcttat ccacttctca 600
 gtatatttttag gtctattgct tggttgaatt ctggagggtcc tgtttgggct 650
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 gtttgaaaaa aaaaaa 766

<210> 258
 <211> 229
 <212> PRT
 <213> Homo sapiens

<400> 258
 Met Thr Cys Cys Glu Gly Trp Thr Ser Cys Asn Gly Phe Ser Leu
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 20 25 30
 Ile Val Ser Leu Val Glu Glu Asp Gln Phe Ser Gln Asn Pro Ile

	35	40	45
Ser Cys Phe Glu Trp Trp Phe Pro Gly Ile Ile Gly Ala Gly Leu	50	55	60
Met Ala Ile Pro Ala Thr Thr Met Ser Leu Thr Ala Arg Lys Arg	65	70	75
Ala Cys Cys Asn Asn Arg Thr Gly Met Phe Leu Ser Ser Phe Phe	80	85	90
Ser Val Ile Thr Val Ile Gly Ala Leu Tyr Cys Met Leu Ile Ser	95	100	105
Ile Gln Ala Leu Leu Lys Gly Pro Leu Met Cys Asn Ser Pro Ser	110	115	120
Asn Ser Asn Ala Asn Cys Glu Phe Ser Leu Lys Asn Ile Ser Asp	125	130	135
Ile His Pro Glu Ser Phe Asn Leu Gln Trp Phe Phe Asn Asp Ser	140	145	150
Cys Ala Pro Pro Thr Gly Phe Asn Lys Pro Thr Ser Asn Asp Thr	155	160	165
Met Ala Ser Gly Trp Arg Ala Ser Ser Phe His Phe Asp Ser Glu	170	175	180
Glu Asn Lys His Arg Leu Ile His Phe Ser Val Phe Leu Gly Leu	185	190	195
Leu Leu Val Gly Ile Leu Glu Val Leu Phe Gly Leu Ser Gln Ile	200	205	210
Val Ile Gly Phe Leu Gly Cys Leu Cys Gly Val Ser Lys Arg Arg	215	220	225
Ser Gln Ile Val			

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 <211> 434
 <212> DNA
 <213> Homo sapiens

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 gctaccaggc ccattgctctt gtctgcccag ctggttgcttc tgagatcaca 150
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 taatccacct ccagaagctc ttgcagccaa gttggaagtg aagcactgca 250
 ccgatcagat atctttttaag aaacgactct cattgaaaaa gtcttggtgg 300
 aaatagttaa aaaatgtggt gtgtgacatg taaaaatgct caacctggtt 350
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tcaacacggtt gctttaataa atcacttgcc ctgc 434

<210> 260

<211> 83

<212> PRT

<213> Homo sapiens

<400> 260

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Ile Thr Val Phe Leu Phe Leu Ser Asp Ala Ala Val Asn Leu Gln
35 40 45

Val Ala Lys Leu Asn Pro Pro Pro Glu Ala Leu Ala Ala Lys Leu
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Glu Val Lys His Cys Thr Asp Gln Ile Ser Phe Lys Lys Arg Leu
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Ser Leu Lys Lys Ser Trp Trp Lys
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<210> 261

<211> 636

<212> DNA

<213> Homo sapiens

<400> 261

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ctgaccaatt gagctgtgag cctggagcag atccgtgggc tgcagacccc 150

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agagagtgac cctggccctt ctctactgg caggcctgac tgccttgga 250

gccaatgacc catttgccaa taaagacgat cccttctact atgactggaa 300

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cagcacagtc ctgtacctga gaaggccatc cactcatca ctccaggctc 450

tgccactact tgctgagcac aggactggcc tccagggatg gcctgaagcc 500

taacactggc cccagcacc tctctccctg ggaggcctta tcctcaagga 550

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ttctttatga attaaactcg cccaccacc cctca 636

<210> 262

<211> 89

<212> PRT

<213> Homo sapiens

1. General Information	
1.1. Name of the project	Project X
1.2. Date of completion	2023-10-27
1.3. Version	1.0.0
1.4. Author	John Doe
1.5. Reviewer	Jane Smith
1.6. Status	Completed
2. Description	
2.1. Purpose	To develop a new software module for data processing.
2.2. Scope	The project includes the design, development, and testing of a new data processing module.
2.3. Objectives	1. Develop a new data processing module. 2. Implement a new data processing module. 3. Test the new data processing module.
2.4. Deliverables	1. New data processing module. 2. Test results.
2.5. Risks	1. Delay in development. 2. Incomplete testing.
2.6. Assumptions	1. Sufficient resources available. 2. Clear requirements.
2.7. Constraints	1. Limited budget. 2. Tight deadline.
2.8. Dependencies	1. Existing software modules. 2. External libraries.
2.9. Milestones	1. Design completion. 2. Development completion. 3. Testing completion.
2.10. Metrics	1. Development time. 2. Testing time. 3. Error rate.
2.11. Tools	1. IDE (Integrated Development Environment). 2. Version control system.
2.12. Standards	1. Industry standards. 2. Company standards.
2.13. Compliance	1. Data protection laws. 2. Software licensing.
2.14. Security	1. Data security. 2. System security.
2.15. Performance	1. Processing speed. 2. Memory usage.
2.16. Usability	1. User interface. 2. Documentation.
2.17. Maintainability	1. Code quality. 2. Documentation.
2.18. Portability	1. Cross-platform compatibility. 2. Hardware independence.
2.19. Scalability	1. Handling large data volumes. 2. Supporting multiple users.
2.20. Reliability	1. Consistent performance. 2. Minimal downtime.
2.21. Flexibility	1. Adapting to changing requirements. 2. Supporting different data formats.
2.22. Interoperability	1. Integrating with existing systems. 2. Supporting different protocols.
2.23. Compatibility	1. Working with different hardware. 2. Supporting different operating systems.
2.24. Accessibility	1. Supporting different languages. 2. Providing user guides.
2.25. Sustainability	1. Long-term support. 2. Regular updates.
2.26. Innovation	1. Implementing new features. 2. Improving performance.
2.27. Research	1. Exploring new technologies. 2. Conducting experiments.
2.28. Development	1. Writing code. 2. Debugging.
2.29. Testing	1. Running tests. 2. Analyzing results.
2.30. Deployment	1. Installing the module. 2. Configuring the system.
2.31. Maintenance	1. Monitoring performance. 2. Fixing bugs.
2.32. Documentation	1. Writing manuals. 2. Creating diagrams.
2.33. Training	1. Providing user guides. 2. Conducting workshops.
2.34. Support	1. Answering user queries. 2. Providing technical assistance.
2.35. Evaluation	1. Assessing user satisfaction. 2. Measuring performance.
2.36. Reporting	1. Generating reports. 2. Presenting findings.
2.37. Communication	1. Keeping stakeholders informed. 2. Collaborating with team members.
2.38. Collaboration	1. Working together. 2. Sharing knowledge.
2.39. Teamwork	1. Supporting each other. 2. Achieving common goals.
2.40. Leadership	1. Guiding the team. 2. Making decisions.
2.41. Management	1. Organizing resources. 2. Controlling costs.
2.42. Planning	1. Setting goals. 2. Creating schedules.
2.43. Execution	1. Implementing plans. 2. Monitoring progress.
2.44. Monitoring	1. Tracking performance. 2. Identifying issues.
2.45. Evaluation	1. Assessing results. 2. Drawing conclusions.
2.46. Reporting	1. Documenting findings. 2. Presenting results.
2.47. Communication	1. Sharing information. 2. Providing feedback.
2.48. Collaboration	1. Working together. 2. Supporting each other.
2.49. Teamwork	1. Supporting each other. 2. Achieving common goals.
2.50. Leadership	1. Guiding the team. 2. Making decisions.
2.51. Management	1. Organizing resources. 2. Controlling costs.
2.52. Planning	1. Setting goals. 2. Creating schedules.
2.53. Execution	1. Implementing plans. 2. Monitoring progress.
2.54. Monitoring	1. Tracking performance. 2. Identifying issues.
2.55. Evaluation	1. Assessing results. 2. Drawing conclusions.
2.56. Reporting	1. Documenting findings. 2. Presenting results.
2.57. Communication	1. Sharing information. 2. Providing feedback.
2.58. Collaboration	1. Working together. 2. Supporting each other.
2.59. Teamwork	1. Supporting each other. 2. Achieving common goals.
2.60. Leadership	1. Guiding the team. 2. Making decisions.
2.61. Management	1. Organizing resources. 2. Controlling costs.
2.62. Planning	1. Setting goals. 2. Creating schedules.
2.63. Execution	1. Implementing plans. 2. Monitoring progress.
2.64. Monitoring	1. Tracking performance. 2. Identifying issues.
2.65. Evaluation	1. Assessing results. 2. Drawing conclusions.
2.66. Reporting	1. Documenting findings. 2. Presenting results.
2.67. Communication	1. Sharing information. 2. Providing feedback.
2.68. Collaboration	1. Working together. 2. Supporting each other.
2.69. Teamwork	1. Supporting each other. 2. Achieving common goals.
2.70. Leadership	1. Guiding the team. 2. Making decisions.
2.71. Management	1. Organizing resources. 2. Controlling costs.
2.72. Planning	1. Setting goals. 2. Creating schedules.
2.73. Execution	1. Implementing plans. 2. Monitoring progress.
2.74. Monitoring	1. Tracking performance. 2. Identifying issues.
2.75. Evaluation	1. Assessing results. 2. Drawing conclusions.
2.76. Reporting	1. Documenting findings. 2. Presenting results.
2.77. Communication	1. Sharing information. 2. Providing feedback.
2.78. Collaboration	1. Working together. 2. Supporting each other.
2.79. Teamwork	1. Supporting each other. 2. Achieving common goals.
2.80. Leadership	1. Guiding the team. 2. Making decisions.
2.81. Management	1. Organizing resources. 2. Controlling costs.
2.82. Planning	1. Setting goals. 2. Creating schedules.
2.83. Execution	1. Implementing plans. 2. Monitoring progress.
2.84. Monitoring	1. Tracking performance. 2. Identifying issues.
2.85. Evaluation	1. Assessing results. 2. Drawing conclusions.
2.86. Reporting	1. Documenting findings. 2. Presenting results.
2.87. Communication	1. Sharing information. 2. Providing feedback.
2.88. Collaboration	1. Working together. 2. Supporting each other.
2.89. Teamwork	1. Supporting each other. 2. Achieving common goals.
2.90. Leadership	1. Guiding the team. 2. Making decisions.
2.91. Management	1. Organizing resources. 2. Controlling costs.
2.92. Planning	1. Setting goals. 2. Creating schedules.
2.93. Execution	1. Implementing plans. 2. Monitoring progress.
2.94. Monitoring	1. Tracking performance. 2. Identifying issues.
2.95. Evaluation	1. Assessing results. 2. Drawing conclusions.
2.96. Reporting	1. Documenting findings. 2. Presenting results.
2.97. Communication	1. Sharing information. 2. Providing feedback.
2.98. Collaboration	1. Working together. 2. Supporting each other.
2.99. Teamwork	1. Supporting each other. 2. Achieving common goals.
2.100. Leadership	1. Guiding the team. 2. Making decisions.

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<211> 1676
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<213> Homo sapiens
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231

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 <212> PRT
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 35 40 45
 Arg Arg Leu Gln Cys Phe Pro Gln Pro Pro Lys Arg Asn Trp Phe
 50 55 60
 Trp Gly His Leu Gly Leu Ile Thr Pro Thr Glu Glu Gly Leu Lys
 65 70 75
 Asp Ser Thr Gln Met Ser Ala Thr Tyr Ser Gln Gly Phe Thr Val
 80 85 90
 Trp Leu Gly Pro Ile Ile Pro Phe Ile Val Leu Cys His Pro Asp
 95 100 105
 Thr Ile Arg Ser Ile Thr Asn Ala Ser Ala Ala Ile Ala Pro Lys
 110 115 120
 Asp Asn Leu Phe Ile Arg Phe Leu Lys Pro Trp Leu Gly Glu Gly
 125 130 135

Ile	Leu	Leu	Ser	Gly	Gly	Asp	Lys	Trp	Ser	Arg	His	Arg	Arg	Met	140	145	150
Leu	Thr	Pro	Ala	Phe	His	Phe	Asn	Ile	Leu	Lys	Ser	Tyr	Ile	Thr	155	160	165
Ile	Phe	Asn	Lys	Ser	Ala	Asn	Ile	Met	Leu	Asp	Lys	Trp	Gln	His	170	175	180
Leu	Ala	Ser	Glu	Gly	Ser	Ser	Arg	Leu	Asp	Met	Phe	Glu	His	Ile	185	190	195
Ser	Leu	Met	Thr	Leu	Asp	Ser	Leu	Gln	Lys	Cys	Ile	Phe	Ser	Phe	200	205	210
Asp	Ser	His	Cys	Gln	Glu	Arg	Pro	Ser	Glu	Tyr	Ile	Ala	Thr	Ile	215	220	225
Leu	Glu	Leu	Ser	Ala	Leu	Val	Glu	Lys	Arg	Ser	Gln	His	Ile	Leu	230	235	240
Gln	His	Met	Asp	Phe	Leu	Tyr	Tyr	Leu	Ser	His	Asp	Gly	Arg	Arg	245	250	255
Phe	His	Arg	Ala	Cys	Arg	Leu	Val	His	Asp	Phe	Thr	Asp	Ala	Val	260	265	270
Ile	Arg	Glu	Arg	Arg	Arg	Thr	Leu	Pro	Thr	Gln	Gly	Ile	Asp	Asp	275	280	285
Phe	Phe	Lys	Asp	Lys	Ala	Lys	Ser	Lys	Thr	Leu	Asp	Phe	Ile	Asp	290	295	300
Val	Leu	Leu	Leu	Ser	Lys	Asp	Glu	Asp	Gly	Lys	Ala	Leu	Ser	Asp	305	310	315
Glu	Asp	Ile	Arg	Ala	Glu	Ala	Asp	Thr	Phe	Met	Phe	Gly	Gly	His	320	325	330
Asp	Thr	Thr	Ala	Ser	Gly	Leu	Ser	Trp	Val	Leu	Tyr	Asn	Leu	Ala	335	340	345
Arg	His	Pro	Glu	Tyr	Gln	Glu	Arg	Cys	Arg	Gln	Glu	Val	Gln	Glu	350	355	360
Leu	Leu	Lys	Asp	Arg	Asp	Pro	Lys	Glu	Ile	Glu	Trp	Asp	Asp	Leu	365	370	375
Ala	Gln	Leu	Pro	Phe	Leu	Thr	Met	Cys	Val	Lys	Glu	Ser	Leu	Arg	380	385	390
Leu	His	Pro	Pro	Ala	Pro	Phe	Ile	Ser	Arg	Cys	Cys	Thr	Gln	Asp	395	400	405
Ile	Val	Leu	Pro	Asp	Gly	Arg	Val	Ile	Pro	Lys	Gly	Ile	Thr	Cys	410	415	420
Leu	Ile	Asp	Ile	Ile	Gly	Val	His	His	Asn	Pro	Thr	Val	Trp	Pro	425	430	435
Asp	Pro	Glu	Val	Tyr	Asp	Pro	Phe	Arg	Phe	Asp	Pro	Glu	Asn	Ser	440	445	450

Lys Gly Arg Ser Pro Leu Ala Phe Ile Pro Phe Ser Ala Gly Pro
455 460 465
Arg Asn Cys Ile Gly Gln Ala Phe Ala Met Ala Glu Met Lys Val
470 475 480
Val Leu Ala Leu Met Leu Leu His Phe Arg Phe Leu Pro Asp His
485 490 495
Thr Glu Pro Arg Arg Lys Leu Glu Leu Ile Met Arg Ala Glu Gly
500 505 510
Gly Leu Trp Leu Arg Val Glu Pro Leu Asn Val Gly Leu Gln
515 520

<210> 265
<211> 584
<212> DNA
<213> Homo sapiens

<400> 265
caacagaagc caagaaggaa gccgtctatc ttgtggcgat catgtataag 50
ctggcctcct gctgtttgct tttcacagga ttcttaaadc ctctcttata 100
tcttcctctc cttgactcca gggaaatata ctttcaactc tcagcacctc 150
atgaagacgc gcgcttaact ccggaggagc tagaaagagc ttcccttcta 200
cagatatattgc cagagatgct ggggtgcagaa agaggggata ttctcaggaa 250
agcagactca agtaccaaca tttttaaccc aagaggaaat ttgagaaagt 300
ttcaggattt ctctggacaa gatcctaaca ttttactgag tcactctttg 350
gccagaatct ggaaaccata caagaaacgt gagactcctg attgcttctg 400
gaaataactgt gtctgaagtg aaataagcat ctgttagtca gctcagaaac 450
acccatctta gaatatgaaa aataacacaa tgcttgattt gaaaacagtg 500
tgagagaaaaa ctaggcaaac tacaccctgt tcattgttac ctggaaaata 550
aatcctctat gttttgcaca aaaaaaaaaa aaaa 584

<210> 266
<211> 124
<212> PRT
<213> Homo sapiens

<400> 266
Met Tyr Lys Leu Ala Ser Cys Cys Leu Leu Phe Thr Gly Phe Leu
1 5 10 15
Asn Pro Leu Leu Ser Leu Pro Leu Leu Asp Ser Arg Glu Ile Ser
20 25 30
Phe Gln Leu Ser Ala Pro His Glu Asp Ala Arg Leu Thr Pro Glu
35 40 45
Glu Leu Glu Arg Ala Ser Leu Leu Gln Ile Leu Pro Glu Met Leu
50 55 60

Gly	Ala	Glu	Arg	Gly	Asp	Ile	Leu	Arg	Lys	Ala	Asp	Ser	Ser	Thr
				65					70					75
Asn	Ile	Phe	Asn	Pro	Arg	Gly	Asn	Leu	Arg	Lys	Phe	Gln	Asp	Phe
				80					85					90
Ser	Gly	Gln	Asp	Pro	Asn	Ile	Leu	Leu	Ser	His	Leu	Leu	Ala	Arg
				95					100					105
Ile	Trp	Lys	Pro	Tyr	Lys	Lys	Arg	Glu	Thr	Pro	Asp	Cys	Phe	Trp
				110					115					120
Lys Tyr Cys Val														

<210> 267
 <211> 654
 <212> DNA
 <213> Homo sapiens

<400> 267
 gaacattttt agttccaag gaatgtacat cagccccacg gaagctaggc 50
 cacctctggtg atgggggttgc tggtttaaaa caaacgccag tcatcctata 100
 taaggacctg acagccacca ggcaccacct ccgccaggaa ctgcaggccc 150
 acctgtctgc aaccagctg aggccatgcc ctccccaggg accgtctgca 200
 gcctcctgct cctcggcatg ctctggctgg acttggccat ggcaggctcc 250
 agcttctctga gccctgaaca ccagagagtc cagcagagaa aggagtcgaa 300
 gaagccacca gccaagctgc agccccgagc tctagcaggc tggctccgcc 350
 cggaagatgg aggtcaagca gaaggggcag aggatgaact ggaagtccgg 400
 ttcaacgccc cttttgatgt tggaatcaag ctgtcagggg ttcagtacca 450
 gcagcacagc caggccctgg ggaagtttct tcaggacatc ctctgggaag 500
 aggccaaaga ggccccagcc gacaagtgat cgcccacaag ccttactcac 550
 ctctctctaa gtttagaagc gctcatctgg cttttcgctt gcttctgcag 600
 caactccac gactgttgta caagctcagg aggcgaataa atgttcaaac 650
 tgta 654

<210> 268
 <211> 117
 <212> PRT
 <213> Homo sapiens

<400> 268
 Met Pro Ser Pro Gly Thr Val Cys Ser Leu Leu Leu Leu Gly Met
 1 5 10 15
 Leu Trp Leu Asp Leu Ala Met Ala Gly Ser Ser Phe Leu Ser Pro
 20 25 30
 Glu His Gln Arg Val Gln Gln Arg Lys Glu Ser Lys Lys Pro Pro
 35 40 45

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Ala	Lys	Leu	Gln	Pro	Arg	Ala	Leu	Ala	Gly	Trp	Leu	Arg	Pro	Glu
				50					55					60
Asp	Gly	Gly	Gln	Ala	Glu	Gly	Ala	Glu	Asp	Glu	Leu	Glu	Val	Arg
				65					70					75
Phe	Asn	Ala	Pro	Phe	Asp	Val	Gly	Ile	Lys	Leu	Ser	Gly	Val	Gln
				80					85					90
Tyr	Gln	Gln	His	Ser	Gln	Ala	Leu	Gly	Lys	Phe	Leu	Gln	Asp	Ile
				95					100					105
Leu	Trp	Glu	Glu	Ala	Lys	Glu	Ala	Pro	Ala	Asp	Lys			
				110					115					

<210> 269
 <211> 1332
 <212> DNA
 <213> Homo sapiens

<400> 269
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 gtccagtacc tcgtgaaccc cgggggtgctc cgcacggacc ccagatgtca 100
 agaatatgaa cacgtggctg ctgttcctcc ccctgttccc ggtgcaggtg 150
 cagaccctga tagtcgtgat catcgggatg ctogtgctcc tgctggactt 200
 tcttggttg gtgcacctgg gccagctgct catcttccac atctacctga 250
 gtatgtcccc caccctaagc ccccgatccc cccaaggctg ggtggtcaga 300
 gctgctcatc ttacacctct acttgagtat gtccctaacc ctgagcccc 350
 cagcctggg gccagagtct ttgtccccg tgtgcgcatg tgttcagggt 400
 cagcctctcc cagaagtgag atcatggaca aaaagggcaa atcacaggaa 450
 gaaattaaat ccatgaggac ccagcaggcc cagcaagaag ctgaactcac 500
 gccgagacct gcaggagtgg tgccaggctg ttgaagtaac aagtttaaaa 550
 tgttcagaga caatggaatg gaatctatta ggcaagaaca ggacattatg 600
 aaataaggac aggtggactt ccaaaaacac aagtagaaat tctaacaatg 650
 aaatatatta caggcaggtc acccactaac caaacaactg aagcgagagc 700
 tgtggtcttg cttggtctca cagtgggcac agcggtaggc ggtcagtcac 750
 gttgctgaac gacggagggt aaactcccca gccccaagaa aacctgtgtt 800
 ggaagtaaca acaacctccc tgctcctggc accagccgtt ttggtcatgg 850
 tgggccagct gcaaagcgtc ttccattctc tgggcagtgg tggccccgag 900
 gctgtggcct ctcaggggggt ttctgtggac acgggcagca gagtgtgtcc 950
 aggccagccc ccaagaatgc cctgctcctg acagcttggc caaccctgg 1000
 tcagggcaga gggagttggg tgggtcaggc tctgggtca cctccatctc 1050

cagagcatcc cctgcctgca gttgtggcaa gaacgcccag ctcagaatga 1100
 acacacccca ccaagagcct ccttggtcat aaccacaggt taccctacaa 1150
 accactgtcc ccacacaacc ctggggatgt tttaaaacac acacctctaa 1200
 cgcatatctt acagtcactg ttgtcttgcc tgaggggtga atttttttta 1250
 atgaaagtgc aatgaaaatc actggattaa atcctacgga cacagagctg 1300
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aa 1332

<210> 270
 <211> 142
 <212> PRT
 <213> Homo sapiens

<400> 270
 Met Asn Thr Trp Leu Leu Phe Leu Pro Leu Phe Pro Val Gln Val
 1 5 10 15
 Gln Thr Leu Ile Val Val Ile Ile Gly Met Leu Val Leu Leu Leu
 20 25 30
 Asp Phe Leu Gly Leu Val His Leu Gly Gln Leu Leu Ile Phe His
 35 40 45
 Ile Tyr Leu Ser Met Ser Pro Thr Leu Ser Pro Arg Ser Pro Gln
 50 55 60
 Gly Trp Val Val Arg Ala Ala His Leu Thr Pro Leu Leu Glu Tyr
 65 70 75
 Val Pro Asn Pro Glu Pro Pro Thr Pro Gly Ala Arg Val Phe Val
 80 85 90
 Pro Arg Val Arg Met Cys Ser Gly Ser Ala Ser Pro Arg Ser Glu
 95 100 105
 Ile Met Asp Lys Lys Gly Lys Ser Gln Glu Glu Ile Lys Ser Met
 110 115 120
 Arg Thr Gln Gln Ala Gln Gln Glu Ala Glu Leu Thr Pro Arg Pro
 125 130 135
 Ala Gly Val Val Pro Gly Ala
 140

<210> 271
 <211> 1484
 <212> DNA
 <213> Homo sapiens

<400> 271
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 accatggcca agatggagct ctgaaggcc ttctctggcc agcggacact 100
 cctatctgcc atcctcagca tgctatcact cagcttctcc acaacatccc 150
 tgctcagcaa ctactggttt gtgggcacac agaaggtgcc caagcccctg 200
 tgcgagaaaag gtctggcagc caagtgcttt gacatgccag tgtccctgga 250

tggagataacc aacacatcca cccaggaggt ggtacaatac aactgggaga 300
 ctgggggatga ccggtttctcc ttccggagct tccggagtgg catgtggcta 350
 tcctgtgagg aaactgtgga agaaccaggg gagagggtgcc gaagtttcat 400
 tgaacttaca ccaccagcca agagagggtga gaaaggacta ctggaatttg 450
 ccacgttgca aggcccatgt caccocactc tccgatttgg agggaagcgg 500
 ttgatggaga aggtttccct cccctccctt cccttggggc tttgtggcaa 550
 aaatcctatg gttatccctg ggaacgcaga tcacctacat cggacttcaa 600
 ttcacagct tcctcctgct actaacagac ttgctactca ctgggaaccc 650
 tgcctgtggg ctcaaactga gcgcctttgc tgctgtttcc tctgtcctgt 700
 caggtctcct ggggatggtg gccacatga tgtattcaca agtcttccaa 750
 gcgactgtca acttgggtcc agaagactgg agaccacatg tttggaatta 800
 tggctggggc ttctacatgg cctggctctc cttcacctgc tgcattggcg 850
 cggctgtcac caccttcaac acgtacacca ggatggtgct ggagttcaag 900
 tgcaagcata gtaagagctt caaggaaaac ccgaactgcc taccacatca 950
 ccatcagtgt ttccctcggc ggctgtcaag tgcagcccc accgtgggtc 1000
 ctttgaccag ctaccaccag tatcataatc agcccatcca ctctgtctct 1050
 gagggagtgc acttctactc cgagctgcgg aacaagggat ttcaaagagg 1100
 ggccagccag gagctgaaag aagcagttag gtcattctgta gaggaagagc 1150
 agtggttagga gttaagcggg tttggggagt aggttgagc cctaccttac 1200
 acgtctgctg attatcaaca tgtgcttaag ccaacatccg tctcttgagc 1250
 atggttttta gaggtacga ataaggctat gaataagggt tatctttaag 1300
 tcctaaggga ttctgggtg ccaactgctct cttttcctct acagctccat 1350
 cttgtttcac ccacccaca tctcacacat ccagaattcc cttctttaot 1400
 gatagtttct gtgccaggtt ctgggctaaa ccatggagat aaaaagaaga 1450
 gtaaaatata cttcccgaac ttaaggatct gaaa 1484

<210> 272
 <211> 285
 <212> PRT
 <213> Homo sapiens

<400> 272
 Met Ala Lys Met Glu Leu Ser Lys Ala Phe Ser Gly Gln Arg Thr
 1 5 10 15
 Leu Leu Ser Ala Ile Leu Ser Met Leu Ser Leu Ser Phe Ser Thr
 20 25 30
 Thr Ser Leu Leu Ser Asn Tyr Trp Phe Val Gly Thr Gln Lys Val

	35	40	45
Pro Lys Pro Leu Cys Glu Lys Gly Leu Ala Ala Lys Cys Phe Asp	50	55	60
Met Pro Val Ser Leu Asp Gly Asp Thr Asn Thr Ser Thr Gln Glu	65	70	75
Val Val Gln Tyr Asn Trp Glu Thr Gly Asp Asp Arg Phe Ser Phe	80	85	90
Arg Ser Phe Arg Ser Gly Met Trp Leu Ser Cys Glu Glu Thr Val	95	100	105
Glu Glu Pro Gly Glu Arg Cys Arg Ser Phe Ile Glu Leu Thr Pro	110	115	120
Pro Ala Lys Arg Gly Glu Lys Gly Leu Leu Glu Phe Ala Thr Leu	125	130	135
Gln Gly Pro Cys His Pro Thr Leu Arg Phe Gly Gly Lys Arg Leu	140	145	150
Met Glu Lys Ala Ser Leu Pro Ser Pro Pro Leu Gly Leu Cys Gly	155	160	165
Lys Asn Pro Met Val Ile Pro Gly Asn Ala Asp His Leu His Arg	170	175	180
Thr Ser Ile His Gln Leu Pro Pro Ala Thr Asn Arg Leu Ala Thr	185	190	195
His Trp Glu Pro Cys Leu Trp Ala Gln Thr Glu Arg Leu Cys Cys	200	205	210
Cys Phe Leu Cys Pro Val Arg Ser Pro Gly Asp Gly Gly Pro His	215	220	225
Asp Val Phe Thr Ser Leu Pro Ser Asp Cys Gln Leu Gly Ser Arg	230	235	240
Arg Leu Glu Thr Thr Cys Leu Glu Leu Trp Leu Gly Leu Leu His	245	250	255
Gly Leu Ala Leu Leu His Leu Leu His Gly Val Gly Cys His His	260	265	270
Leu Gln His Val His Gln Asp Gly Ala Gly Val Gln Val Gln Ala	275	280	285

<210> 273
 <211> 1158
 <212> DNA
 <213> Homo sapiens

<400> 273
 aactggaagg aaagaaagaa aggtcagctt tggcccagat gtggttaccc 50
 cttggtctcc tgtctttatg tctttctcct cttcctattc tgtcatctcc 100
 ctcacttaag tctcaggcct gtcagcagct cctgtggaca ttgccatccc 150
 ctctggtagc cttcagagca aacaggacaa cctatgttat ggatgtttcc 200

<210> 275
<211> 2694
<212> DNA
<213> Homo sapiens

<400> 275
gtagcgcgtc ttgggtctcc cggtgccgc tgctgccgc gccgcctcgg 50
gtcgtggagc caggagcgac gtcaccgcca tggcaggcat caaagctttg 100
attagtttgt cctttggagg agcaatcgga ctgatgtttt tgatgcttgg 150
atgtgccctt ccaatataca acaaatactg gcccctcttt gttctatttt 200
tttacatcct ttcacctatt ccatactgca tagcaagaag attagtggat 250
gatacagatg ctatgagtaa cgcttgtaag gaacttgcca tctttcttac 300
aacgggcatt gtcgtgtcag cttttggact ccctattgta tttgccagag 350
cacatctgat tgagtgggga gcttgtgcac ttgttctcac aggaaacaca 400
gtcatctttg caactatact aggccttttc ttggtctttg gaagcaatga 450
cgacttcagc tggcagcagt ggtgaaaaga aattactgaa ctattgtcaa 500
atggacttcc tgtcatttgt tggccattca cgcacacagg agatggggca 550
gttaatgctg aatggtatag caagcctctt gggggatatt taggtgctcc 600
cttctcactt ttattgtaag catactatct tcacagagac ttgctgaagg 650
attaaaagga ttttctcttt tggaaaagct tgactgattt cacacttatt 700
tatagtatgc tttttgtggt gtctgtctga atttaaatat ttatgtgttt 750
ttcctgttag gttgattttt tttggaatca atatgcaatg ttaaacaact 800
ttttaatgta atcatttgca ttggttagga attcagaatt ccgccggctc 850
tattactggt caagtacatc ttttctctta aaattattta gcctccatta 900
ttacaaaaaa ttataaaaat aagttttcag tcagtcagga tgacatcact 950
cccaatgtta tgcagacata cagacggttg gcatacgta tagactgtat 1000
actcagtgca aatatagctg catttatacc tcagaggggc caagtgttaa 1050
tgcccatgcc ctccgttaag gggtgttggg tttactggta gacagatgtt 1100
ttgtggattg aaaattattt tatggaattg ctacagagga gtgcttttct 1150
tctcaattgt tagaagaatt tatgttaaac ttttaaggtaa ggggtgtaaaa 1200
acatttttga gataagggtt ttatttatgt ttattattgt tagagtgagt 1250
tgcaatgtgg gaagaaatga cattgaaatt ccagtttttg aatcctgttt 1300
ctattttataa gtgaaatttg tgatctccta tcaacctttc atgttttacc 1350
ctgttaaaat ggacatacat ggaaccacta ctgatgaggg acagttgtat 1400
gtttgcatca tatatgccag aaaaccttcc tctgcttctt ccttttgact 1450

tatttggtat gttgtatata ttacataaaa taacttttca aatatagttt 1500
aataacactt agaagtgttt acttacctgg aaaataattg ctatgccgta 1550
cattcagagt gccccctccc ctgcaaggcc ttgccatgat taacaagtaa 1600
cttggttagtc ttacagataa ttcattgcatt aacagtttaa gatttagacc 1650
atggtaatag tagttcttat tctctaaggt tatatcatat gtaattttaa 1700
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gagttaatgc aaagtagcca agtccagcta tatagcagct tcagaaacat 1850
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gtttacatct aataattatc aggacttttt tcaggagtgg gttataaaaa 1950
cattcaagtt ggtctgacag tattttgtta aggatatttg tttgtatggt 2000
tattcagtat acttacataa aaattatttc gccatcagcc aaaactcagt 2050
aatcatgaca gctgtctgtt gttttatgaa gtttatttct caagaaaatg 2100
ggaataaatt tgggatttgt tcagcttttt tactaaagat gcctaaagcc 2150
acagggtttta ttgcctaact taagccatga cttttagata tgagatgacg 2200
ggaagcagga cgaaatatcg gcgtgtggct ggagccttcc cactggaggc 2250
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cctattttct gttctggatg tcagtgcagt gcactgctac tgttttatcc 2450
acttggccac agactttttc taacagctgc gtattatttc tatatactaa 2500
ttgcattggc agcatttgtt ctttgacctt gtatactagc ttgacatagt 2550
gctgtctctg atttctaggc tagttacttg agatatgaat tttccataga 2600
atatgcactg atacaacatt accattcttc tatggaaaga aaacttttga 2650
tgatgaaaca ataaagattt taaatatcta ttttaaaaaa aaaa 2694

<210> 276
<211> 131
<212> PRT
<213> Homo sapiens

<400> 276
Met Ala Gly Ile Lys Ala Leu Ile Ser Leu Ser Phe Gly Gly Ala
1 5 10 15
Ile Gly Leu Met Phe Leu Met Leu Gly Cys Ala Leu Pro Ile Tyr
20 25 30
Asn Lys Tyr Trp Pro Leu Phe Val Leu Phe Phe Tyr Ile Leu Ser

	35		40		45
Pro Ile Pro Tyr Cys Ile Ala Arg Arg Leu Val Asp Asp Thr Asp	50		55		60
Ala Met Ser Asn Ala Cys Lys Glu Leu Ala Ile Phe Leu Thr Thr	65		70		75
Gly Ile Val Val Ser Ala Phe Gly Leu Pro Ile Val Phe Ala Arg	80		85		90
Ala His Leu Ile Glu Trp Gly Ala Cys Ala Leu Val Leu Thr Gly	95		100		105
Asn Thr Val Ile Phe Ala Thr Ile Leu Gly Phe Phe Leu Val Phe	110		115		120
Gly Ser Asn Asp Asp Phe Ser Trp Gln Gln Trp	125		130		

<210> 277
 <211> 4104
 <212> DNA
 <213> Homo sapiens

<400> 277
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 caogcgctcg cccacgcgtc cgcccacgcg tccggtgcaa gctcgcgccg 100
 cacactgcct ggtggaggga aggagcccgg gcgcctctcg ccgctccccg 150
 cgccgcgcgtc cgcacctccc caccgcccgc cgcccgccgc ccgcccggcg 200
 caaagcatga gtgagcccgc tctctgcagc tgcccggggc gcgaatggca 250
 ggctgtttcc gcggagtaaa aggtggcgcc ggtcagtggc cgtttccaat 300
 gacggacatt aaccagactg tcagatcctg gggagtcgcg agccccgagt 350
 ttggagtttt tccccccac aacgtcacag tccgaactgc agagggaaag 400
 gaaggcggca ggaaggcgaa gctcgggctc cggcacgtag ttgggaaact 450
 tgccgggtcct agaagtcgcc tccccgcctt gccggccgcc cttgcagccc 500
 cgagccgagc agcaaagtga gacattgtgc gcctgccaga tccgccggcc 550
 gcggaccggg gctgcctcgg aaacacagag gggctcttctc tcgccctgca 600
 tataattagc ctgcacacaa agggagcagc tgaatggagg ttgtcactct 650
 ctggaaaagg atttctgacc gagcgcttcc aatggacatt ctccagtctc 700
 tctggaaaaga ttctcgctaa tggatttctt gctgctcggc ctctgtctat 750
 actggctgct gaggaggccc tcgggggtgg tcttgtgtct gctggggggc 800
 tgctttcaga tgctgcccgc cgccccagc ggggtgcccgc agctgtgccg 850
 gtgcgagggg cggtctgtgt actgcgaggc gctcaacctc accgaggcgc 900
 cccacaacct gtccggcctg ctgggcttgt ccctgcgcta caacagcctc 950

tcggagctgc gcgccggcca gttcacgggg ttaatgcagc tcacgtggct 1000
ctatctggat cacaatcaca tctgctccgt gcagggggac gcctttcaga 1050
aactgcgccg agttaaggaa ctcacgctga gttccaacca gatcacccaa 1100
ctgcccaca ccaccttccg gcccatgccc aacctgcgca gcgtggacct 1150
ctcgtacaac aagctgcagg cgctcgcgcc cgacctcttc cacgggctgc 1200
ggaagctcac cacgctgcat atgcggggcca acgccatcca gtttgtgccc 1250
gtgcgcatct tccaggactg ccgcagcctc aagtttctcg acatcgata 1300
caatcagctc aagagtctgg cgcgcaactc tttcgccggc ttgtttaagc 1350
tcaccgagct gcacctcgag cacaacgact tggtaagggt gaacttcgcc 1400
cacttcccgc gcctcatctc cctgcactcg ctctgcctgc ggaggaacaa 1450
ggtggccatt gtggtcagct cgctggactg ggtttggaac ctggagaaaa 1500
tggaacttgc gggcaacgag atcgagtaca tggagcccca tgtgttcgag 1550
accgtgccgc acctgcagtc cctgcagctg gactccaacc gcctcaccta 1600
catcgagccc cggatcctca actcttgaa gtccctgaca agcatcacc 1650
tggcgggaa cctgtgggat tgcgggcgca acgtgtgtgc cctagcctcg 1700
tggtctagca acttccaggg gcgctacgat ggcaacttgc agtgcgccag 1750
cccgagtagc gcacagggcg aggacgtcct ggacgccgtg tacgccttcc 1800
acctgtgcga ggatggggcc gagcccacca gcggccacct gctctggcc 1850
gtcaccaacc gcagtgatct ggggccccct gccagctcgg ccaccacgct 1900
cgcgagcggc ggggaggggc agcacgacgg cacattcgag cctgccaccg 1950
tggtcttcc agggcgag cagccgaga acgccgtgca gatccacaag 2000
gtggtcacgg gcaccatggc cctcatcttc tcttctctca tctgtgctct 2050
ggtgctctac gtgtcctgga agtggttccc agccagcctc aggagctca 2100
gacagtgctt tgtcacgcag cgcaggaagc aaaagcagaa acagaccatg 2150
catcagatgg ctgccatgtc tgcccaggaa tactacgttg attacaaacc 2200
gaaccacatt gagggagccc tggatgatcat caacgagtat ggctcgtgta 2250
cctgccacca gcagcccgcg agggaatgcg aggtgtgatt gtcccagtgg 2300
ctctcaaccc atgcgctacc aaatacgctt gggcagccgg gacgggcccg 2350
cgggcaccag gctggggctc ccttgtctgt gctctgatat gctccttgac 2400
tgaaaacttta aggggatctc tcccagagac ttgacatttt agctttattg 2450
tgtcttaaaa acaaaagcga attaaaacac aacaaaaaac cccacccac 2500
aaccttcagg acagtctatc ttaaatttca tatgagaact ccttctctcc 2550

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 ataagacaga gagagaataa tcgtgctttg ttttatgcta ctccctccac 2650
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 atttcatgaa gaaccattgg aaagaggaat ctgcaatctg ggagcttaag 2750
 agcaaatgat gaccatagaa agctatgttc ttactttgtg tgtgtgtctg 2800
 tatgtttctg cgttgtgtgt cttttagtagc aagcaaacgt tgtctacaca 2850
 aacgggaatt tagctcacat catttcatgc ccctgtgcct ctagctctgg 2900
 agattggtgg ggggaggtgg ggggaaacgg caggaataag ggaaagtgg 2950
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 attatcttta agcttcaaga aacttgctct gacccctcta agcaaactac 3050
 taagcattta aaagagaatc taatttttaa aggtgtagca cctttttttt 3100
 tattcttccc acagaggtg ctaatctcat tatgtgtgc tatctgaaaa 3150
 gaacttaagg ccacaattca cgtctcgtcc tgggcattgt gatggattga 3200
 ccctccattt gcagtacctt cccagctgat taaagttcag cagtggatt 3250
 gaggtttttc gaatatttat atagaaaaaa agtcttttca catgacaaat 3300
 gacactctca caccagtctt agccctagta gtttttttagg ttggaccaga 3350
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 taccacaat gcagcctata ctccaagac tacaaagtta ccatcgcaaa 3500
 ggaaaggtta ttccagtaaa aggaaatagt tttctcaacc atttaaaaaat 3550
 attcttctga actcatcaaa gtagaagagc cccaacctt ttctctctgc 3600
 cttcaagaag gcagacattt ggtatgattt agcatcaaca acacatttat 3650
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 agttttccaa gcaagtacac acagatctct ggtaggatta ggggccactt 3750
 gtgtttccgg cttatttttag tcgacttgtc agcaagtgtg atgcctagtc 3800
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 tagaaggaa atcatcacat acccctctca cagagaaaat tatcaaagaa 3900
 ccagaaatta tatctgtttt ggagcaagag tgtcataatg tttcagggtg 3950
 gtcaaaataa acataaatta tctcctctag atgagtggcg atgttggtg 4000
 atttgggtct gccattgaca gaatgtcaaa taaaaggaa ttagctagaa 4050
 tatgaccatt aaatgtgctt ctgaaatata ttttgagata ggtttagaat 4100
 gtca 4104

<210> 278
 <211> 522
 <212> PRT
 <213> Homo sapiens

<400> 278

Met	Asp	Phe	Leu	Leu	Leu	Gly	Leu	Cys	Leu	Tyr	Trp	Leu	Leu	Arg	1	5	10	15
Arg	Pro	Ser	Gly	Val	Val	Leu	Cys	Leu	Leu	Gly	Ala	Cys	Phe	Gln	20	25	30	
Met	Leu	Pro	Ala	Ala	Pro	Ser	Gly	Cys	Pro	Gln	Leu	Cys	Arg	Cys	35	40	45	
Glu	Gly	Arg	Leu	Leu	Tyr	Cys	Glu	Ala	Leu	Asn	Leu	Thr	Glu	Ala	50	55	60	
Pro	His	Asn	Leu	Ser	Gly	Leu	Leu	Gly	Leu	Ser	Leu	Arg	Tyr	Asn	65	70	75	
Ser	Leu	Ser	Glu	Leu	Arg	Ala	Gly	Gln	Phe	Thr	Gly	Leu	Met	Gln	80	85	90	
Leu	Thr	Trp	Leu	Tyr	Leu	Asp	His	Asn	His	Ile	Cys	Ser	Val	Gln	95	100	105	
Gly	Asp	Ala	Phe	Gln	Lys	Leu	Arg	Arg	Val	Lys	Glu	Leu	Thr	Leu	110	115	120	
Ser	Ser	Asn	Gln	Ile	Thr	Gln	Leu	Pro	Asn	Thr	Thr	Phe	Arg	Pro	125	130	135	
Met	Pro	Asn	Leu	Arg	Ser	Val	Asp	Leu	Ser	Tyr	Asn	Lys	Leu	Gln	140	145	150	
Ala	Leu	Ala	Pro	Asp	Leu	Phe	His	Gly	Leu	Arg	Lys	Leu	Thr	Thr	155	160	165	
Leu	His	Met	Arg	Ala	Asn	Ala	Ile	Gln	Phe	Val	Pro	Val	Arg	Ile	170	175	180	
Phe	Gln	Asp	Cys	Arg	Ser	Leu	Lys	Phe	Leu	Asp	Ile	Gly	Tyr	Asn	185	190	195	
Gln	Leu	Lys	Ser	Leu	Ala	Arg	Asn	Ser	Phe	Ala	Gly	Leu	Phe	Lys	200	205	210	
Leu	Thr	Glu	Leu	His	Leu	Glu	His	Asn	Asp	Leu	Val	Lys	Val	Asn	215	220	225	
Phe	Ala	His	Phe	Pro	Arg	Leu	Ile	Ser	Leu	His	Ser	Leu	Cys	Leu	230	235	240	
Arg	Arg	Asn	Lys	Val	Ala	Ile	Val	Val	Ser	Ser	Leu	Asp	Trp	Val	245	250	255	
Trp	Asn	Leu	Glu	Lys	Met	Asp	Leu	Ser	Gly	Asn	Glu	Ile	Glu	Tyr	260	265	270	
Met	Glu	Pro	His	Val	Phe	Glu	Thr	Val	Pro	His	Leu	Gln	Ser	Leu	275	280	285	

Gln	Leu	Asp	Ser	Asn	Arg	Leu	Thr	Tyr	Ile	Glu	Pro	Arg	Ile	Leu
				290					295					300
Asn	Ser	Trp	Lys	Ser	Leu	Thr	Ser	Ile	Thr	Leu	Ala	Gly	Asn	Leu
				305					310					315
Trp	Asp	Cys	Gly	Arg	Asn	Val	Cys	Ala	Leu	Ala	Ser	Trp	Leu	Ser
				320					325					330
Asn	Phe	Gln	Gly	Arg	Tyr	Asp	Gly	Asn	Leu	Gln	Cys	Ala	Ser	Pro
				335					340					345
Glu	Tyr	Ala	Gln	Gly	Glu	Asp	Val	Leu	Asp	Ala	Val	Tyr	Ala	Phe
				350					355					360
His	Leu	Cys	Glu	Asp	Gly	Ala	Glu	Pro	Thr	Ser	Gly	His	Leu	Leu
				365					370					375
Ser	Ala	Val	Thr	Asn	Arg	Ser	Asp	Leu	Gly	Pro	Pro	Ala	Ser	Ser
				380					385					390
Ala	Thr	Thr	Leu	Ala	Asp	Gly	Gly	Glu	Gly	Gln	His	Asp	Gly	Thr
				395					400					405
Phe	Glu	Pro	Ala	Thr	Val	Ala	Leu	Pro	Gly	Gly	Glu	His	Ala	Glu
				410					415					420
Asn	Ala	Val	Gln	Ile	His	Lys	Val	Val	Thr	Gly	Thr	Met	Ala	Leu
				425					430					435
Ile	Phe	Ser	Phe	Leu	Ile	Val	Val	Leu	Val	Leu	Tyr	Val	Ser	Trp
				440					445					450
Lys	Cys	Phe	Pro	Ala	Ser	Leu	Arg	Gln	Leu	Arg	Gln	Cys	Phe	Val
				455					460					465
Thr	Gln	Arg	Arg	Lys	Gln	Lys	Gln	Lys	Gln	Thr	Met	His	Gln	Met
				470					475					480
Ala	Ala	Met	Ser	Ala	Gln	Glu	Tyr	Tyr	Val	Asp	Tyr	Lys	Pro	Asn
				485					490					495
His	Ile	Glu	Gly	Ala	Leu	Val	Ile	Ile	Asn	Glu	Tyr	Gly	Ser	Cys
				500					505					510
Thr	Cys	His	Gln	Gln	Pro	Ala	Arg	Glu	Cys	Glu	Val			
				515					520					

<210> 279

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 279

tccgtgcagg gggacgcctt tcagaaactg cgccgagtta aggaac 46

<210> 280

<211> 709

<212> DNA

<213> Homo sapiens

<400> 280
 gtgcaaggag ccgaggcgag atgggcgtcc tgggccgggt cctgctgtgg 50
 ctgcagctct gcgcactgac ccaggcggtc tccaaactct ggggtcccaa 100
 caccgacttc gacgtcgag ccaactggag ccagaaccgg accccgtgcg 150
 ccggcggcgc cgttgagttc ccggcggaca agatgggtgtc agtcctggtg 200
 caagaaggtc acgccgtctc agacatgctc ctgccgctgg atggggaact 250
 cgtcctgggt tcaggagccg gattcggcgt ctcagacgtg ggctcgacc 300
 tggactgtgg cgccggcgaa cctgccgtct tccgcgactc tgaccgcttc 350
 tcctggcatg acccgcacct gtggcgctct ggggacgagg cacctggcct 400
 cttcttcgtg gacgccgagc gcgtgccctg ccgccacgac gacgtcttct 450
 ttccgcctag tgctccttc cgcgtggggc tcggccctgg cgctagcccc 500
 gtgcgtgtcc gcagcatctc ggctctgggc cggacgttca cgcgcgacga 550
 ggacctgggt gttttcctgg cgtcccgcgc gggccgccta cgcttcacg 600
 ggccggggcgc gctgagcgtg ggccccgagg actgcgcgga cccgtcgggc 650
 tgcgtctgcg gcaacgcgga ggccgagccg tggatctgcg cggccctgct 700
 ccagcccct 709

<210> 281
 <211> 229
 <212> PRT
 <213> Homo sapiens

<400> 281
 Met Gly Val Leu Gly Arg Val Leu Leu Trp Leu Gln Leu Cys Ala
 1 5 10 15
 Leu Thr Gln Ala Val Ser Lys Leu Trp Val Pro Asn Thr Asp Phe
 20 25 30
 Asp Val Ala Ala Asn Trp Ser Gln Asn Arg Thr Pro Cys Ala Gly
 35 40 45
 Gly Ala Val Glu Phe Pro Ala Asp Lys Met Val Ser Val Leu Val
 50 55 60
 Gln Glu Gly His Ala Val Ser Asp Met Leu Leu Pro Leu Asp Gly
 65 70 75
 Glu Leu Val Leu Ala Ser Gly Ala Gly Phe Gly Val Ser Asp Val
 80 85 90
 Gly Ser His Leu Asp Cys Gly Ala Gly Glu Pro Ala Val Phe Arg
 95 100 105
 Asp Ser Asp Arg Phe Ser Trp His Asp Pro His Leu Trp Arg Ser
 110 115 120
 Gly Asp Glu Ala Pro Gly Leu Phe Phe Val Asp Ala Glu Arg Val
 125 130 135

Pro	Cys	Arg	His	Asp	Asp	Val	Phe	Phe	Pro	Pro	Ser	Ala	Ser	Phe
				140					145					150
Arg	Val	Gly	Leu	Gly	Pro	Gly	Ala	Ser	Pro	Val	Arg	Val	Arg	Ser
				155					160					165
Ile	Ser	Ala	Leu	Gly	Arg	Thr	Phe	Thr	Arg	Asp	Glu	Asp	Leu	Ala
				170					175					180
Val	Phe	Leu	Ala	Ser	Arg	Ala	Gly	Arg	Leu	Arg	Phe	His	Gly	Pro
				185					190					195
Gly	Ala	Leu	Ser	Val	Gly	Pro	Glu	Asp	Cys	Ala	Asp	Pro	Ser	Gly
				200					205					210
Cys	Val	Cys	Gly	Asn	Ala	Glu	Ala	Gln	Pro	Trp	Ile	Cys	Ala	Ala
				215					220					225

Leu Leu Gln Pro

<210> 282
 <211> 644
 <212> DNA
 <213> Homo sapiens

<400> 282
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 gaagcgaatg tttgagccta ctcgtttgat tgcaactatc atgggtgctgt 100
 tgtgttttgc acttaccctg tgttctgcct tttggtggca taacaaggga 150
 cttgcactta tcttctgcat tttgcagtct ttggcattga cgtggtacag 200
 cctttccttc ataccatttg caagggatgc tgtgaagaag tgttttgccg 250
 tgtgtcttgc ataattcatg gccagtttta tgaagctttg gaaggcacta 300
 tggacagaag ctggtggaca gttttgtaac tatcttcgaa acctctgtct 350
 tacagacatg tgccttttat cttgcagcaa tgtgttgctt gtgattcgaa 400
 catttgaggg ttacttttgg aagcaacaat acattctcga acctgaatgt 450
 cagtagcaca ggatgagaag tgggttctgt atcttgtgga gtggaatctt 500
 cctcatgtac ctgtttcctc tctggatgtt gtccactga attcccatga 550
 atacaaacct attcagcaac agcaaaaaaa aaaaaaaaaa aaaaaaaaaa 600
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 644

<210> 283
 <211> 77
 <212> PRT
 <213> Homo sapiens

<400> 283
 Met Gly Pro Val Lys Gln Leu Lys Arg Met Phe Glu Pro Thr Arg
 1 5 10 15
 Leu Ile Ala Thr Ile Met Val Leu Leu Cys Phe Ala Leu Thr Leu

	20		25		30
Cys Ser Ala Phe Trp Trp His Asn Lys Gly Leu Ala Leu Ile Phe					
	35		40		45
Cys Ile Leu Gln Ser Leu Ala Leu Thr Trp Tyr Ser Leu Ser Phe					
	50		55		60
Ile Pro Phe Ala Arg Asp Ala Val Lys Lys Cys Phe Ala Val Cys					
	65		70		75
Leu Ala					

<210> 284
 <211> 2623
 <212> DNA
 <213> Homo sapiens

<400> 284
 ttgagcgcag gtgagctcct ggcggttccg ggggcgttcc tccagtcacc 50
 ctcccgcggt taccgcggc ggcggcagg gagtctctc cagaccctcc 100
 ctcccggttg tccaaactaa tacggactga acggatcgct gcgaggggtg 150
 gagagaaaat tagggggaga aaggacagag agagcaacta ccatccatag 200
 ccagatagat tatcttacac tgaactgatc aagtactttg aaaatgactt 250
 cgaaatttat cttggtgtcc ttcatacttg ctgcactgag tctttcaacc 300
 accttttctc tccaactaga ccagcaaaag gttctactag tttcttttga 350
 tggattccgt tgggattact tatataaagt tccaacgccc cattttcatt 400
 atattatgaa atatgggtgtt cacgtgaagc aagttactaa tgtttttatt 450
 acaaaaacct accctaacca ttatactttg gtaactggcc tctttgcaga 500
 gaatcatggg attgttgcaa atgatatgtt tgatcctatt cggaacaaat 550
 ctttctcctt ggatcacatg aatatttatg attccaagtt ttgggaagaa 600
 gcgacaccaa tatggatcac aaaccagagg gcaggacata ctagtgggtg 650
 agccatgtgg ccggaacag atgtaaaaat acataagcgc tttcctactc 700
 attacatgcc ttacaatgag tcagtttcat ttgaagatag agttgccaaa 750
 attgttgaat ggtttacgtc aaaagagccc ataaatcttg gtcttctcta 800
 ttgggaagac cctgatgaca tgggccacca tttgggacct gacagtccgc 850
 tcatggggcc tgtcatttca gatattgaca agaagttagg atatctcata 900
 caaatgctga aaaaggcaaa gttgtggaac actctgaacc taatcatcac 950
 aagtgatcat ggaatgacgc agtgctctga ggaaaggtta atagaacttg 1000
 accagtacct ggataaagac cactataccc tgattgatca atctccagta 1050
 gcagccatct tgccaaaaga aggtaaattt gatgaagtct atgaagcact 1100

290	295	300
Val Pro Glu Arg Trp His Tyr Lys Tyr	Asn Ser Arg Ile Gln Pro	
305	310	315
Ile Ile Ala Val Ala Asp Glu Gly Trp	His Ile Leu Gln Asn Lys	
320	325	330
Ser Asp Asp Phe Leu Leu Gly Asn His	Gly Tyr Asp Asn Ala Leu	
335	340	345
Ala Asp Met His Pro Ile Phe Leu Ala	His Gly Pro Ala Phe Arg	
350	355	360
Lys Asn Phe Ser Lys Glu Ala Met Asn	Ser Thr Asp Leu Tyr Pro	
365	370	375
Leu Leu Cys His Leu Leu Asn Ile Thr	Ala Met Pro His Asn Gly	
380	385	390
Ser Phe Trp Asn Val Gln Asp Leu Leu	Asn Ser Ala Met Pro Arg	
395	400	405
Val Val Pro Tyr Thr Gln Ser Thr Ile	Leu Leu Pro Gly Ser Val	
410	415	420
Lys Pro Ala Glu Tyr Asp Gln Glu Gly	Ser Tyr Pro Tyr Phe Ile	
425	430	435
Gly Val Ser Leu Gly Ser Ile Ile Val	Ile Val Phe Phe Val Ile	
440	445	450
Phe Ile Lys His Leu Ile His Ser Gln	Ile Pro Ala Leu Gln Asp	
455	460	465
Met His Ala Glu Ile Ala Gln Pro Leu	Leu Gln Ala	
470	475	

<210> 286
 <211> 1337
 <212> DNA
 <213> Homo sapiens

<400> 286
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 cgaggaggccc aggacaggcc caccctgcgg ggcgggaggc agccggggtg 100
 agggaggtga agaaaccaag acgcagagag gccaagcccc ttgccttggg 150
 tcacacagcc aaaggaggca gagccagaac tcacaaccag atccagaggc 200
 aacagggaca tggccacctg ggacgaaaag gcagtcaccc gcagggccaa 250
 ggtggctccc gctgagagga tgagcaagtt ctttaaggcac ttcacggtcg 300
 tgggagacga ctaccatgcc tggaacatca actacaagaa atgggagaat 350
 gaagaggagg aggaggagga ggagcagcca ccacccacac cagtctcagg 400
 cgaggaaggc agagctgcag cccctgacgt tgcccctgcc cctggccccg 450
 caccagggc ccccttgac ttcaggggca tggtgaggaa actgttcagc 500

tcccacaggt ttcaggtcat catcatctgc ttggtggttc tggatgccct 550
cctggtgctt gctgagctca tcctggacct gaagatcatc cagcccgaca 600
agaataacta tgctgccatg gtattccact acatgagcat caccatcttg 650
gtctttttta tgatggagat catctttaaa ttatttgtct tccgcctgag 700
ttctttcacc acaagtttga gatcctggat gcccgtcgtg gtggtggtct 750
cattcatcct ggacattgtc ctctgttcc aggagcacca gtttgaggct 800
ctgggcctgc tgattctgct ccggtgtggt cgggtggccc ggatcatcaa 850
tggtgattatc atctcagtta agacacgttc agaacggcaa ctcttaaggt 900
taaaacagat gaatgtacaa ttggccgcca agattcaaca ccttgagttc 950
agctgctctg agaagcccct ggactgatga gtttgctgta tcaacctgta 1000
aggagaagct ctctccgat ggctatggga atgaaagaat ccgacttcta 1050
ctctcacaca gccaccgtga aagtcctgga gtaaaatgtg ctgtgtacag 1100
aagagagaga aggaagcagg ctggcatgtt cactgggctg gtgttacgac 1150
agagaacctg acagtcactg gccagttatc acttcagatt acaaatacaca 1200
cagagcatct gcctgttttc aatcacaga gaacaaaacc aaaatctata 1250
aagatattct gaaaatatga cagaatttga caaataaaaag cataaacgtg 1300
taaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 1337

<210> 287
<211> 255
<212> PRT
<213> Homo sapiens

<400> 287
Met Ala Thr Trp Asp Glu Lys Ala Val Thr Arg Arg Ala Lys Val
1 5 10 15
Ala Pro Ala Glu Arg Met Ser Lys Phe Leu Arg His Phe Thr Val
20 25 30
Val Gly Asp Asp Tyr His Ala Trp Asn Ile Asn Tyr Lys Lys Trp
35 40 45
Glu Asn Glu Glu Glu Glu Glu Glu Glu Gln Pro Pro Pro Thr
50 55 60
Pro Val Ser Gly Glu Glu Gly Arg Ala Ala Ala Pro Asp Val Ala
65 70 75
Pro Ala Pro Gly Pro Ala Pro Arg Ala Pro Leu Asp Phe Arg Gly
80 85 90
Met Leu Arg Lys Leu Phe Ser Ser His Arg Phe Gln Val Ile Ile
95 100 105
Ile Cys Leu Val Val Leu Asp Ala Leu Leu Val Leu Ala Glu Leu
110 115 120

Ile	Leu	Asp	Leu	Lys	Ile	Ile	Gln	Pro	Asp	Lys	Asn	Asn	Tyr	Ala
				125					130					135
Ala	Met	Val	Phe	His	Tyr	Met	Ser	Ile	Thr	Ile	Leu	Val	Phe	Phe
				140					145					150
Met	Met	Glu	Ile	Ile	Phe	Lys	Leu	Phe	Val	Phe	Arg	Leu	Ser	Ser
				155					160					165
Phe	Thr	Thr	Ser	Leu	Arg	Ser	Trp	Met	Pro	Val	Val	Val	Val	Val
				170					175					180
Ser	Phe	Ile	Leu	Asp	Ile	Val	Leu	Leu	Phe	Gln	Glu	His	Gln	Phe
				185					190					195
Glu	Ala	Leu	Gly	Leu	Leu	Ile	Leu	Leu	Arg	Leu	Trp	Arg	Val	Ala
				200					205					210
Arg	Ile	Ile	Asn	Gly	Ile	Ile	Ile	Ser	Val	Lys	Thr	Arg	Ser	Glu
				215					220					225
Arg	Gln	Leu	Leu	Arg	Leu	Lys	Gln	Met	Asn	Val	Gln	Leu	Ala	Ala
				230					235					240
Lys	Ile	Gln	His	Leu	Glu	Phe	Ser	Cys	Ser	Glu	Lys	Pro	Leu	Asp
				245					250					255

<210> 288
 <211> 3334
 <212> DNA
 <213> Homo sapiens

<400> 288
 cggctcgagc tcgagccgaa tcggctcgag gggcagtgga gcacccagca 50
 ggccgccaac atgctctgtc tgtgcctgta cgtgccggtc atcggggaag 100
 cccagaccga gttccagtac tttgagtcga aggggctccc tgccgagctg 150
 aagtccattt tcaagctcag tgtcttcac cctcccagg aattctccac 200
 ctaccgccag tggaagcaga aaattgtaca agctggagat aaggaccttg 250
 atgggcagct agactttgaa gaatttgtcc attatctcca agatcatgag 300
 aagaagctga ggctggtggt taagattttg gacaaaaaga atgatggacg 350
 cattgacgag caggagatca tgcagtcctt gcgggacttg ggagtcaaga 400
 tatctgaaca gcaggcagaa aaaatttctca agagcatgga taaaaacggc 450
 acgatgacca tcgactggaa cgagtggaga gactaccacc tcctccaccc 500
 cgtggaaaac atccccgaga tcatcctcta ctggaagcat tccacgatct 550
 ttgatgtggg tgagaatcta acggtcccgg atgagttcac agtggaggag 600
 aggcagacgg ggatgtggtg gagacacctg gtggcaggag gtggggcagg 650
 ggccgtatcc agaacctgca cggccccctt ggacaggctc aaggtgctca 700
 tgcagggtcca tgcctcccgag agcaacaaca tgggcatcgt tgggtggcttc 750

actcagatga ttcgagaagg agggggccagg tcactctggc ggggcaatgg 800
catcaacgtc ctcaaaattg cccccgaatc agccatcaaa ttcattggcct 850
atgagcagat caagcgcctt gttggtagt accaggagac tctgaggatt 900
cacgagaggc ttgtggcagg gtccttggca gggggccatcg cccagagcag 950
catctacca atggagggtc tgaagaccg gatggcgctg cggaagacag 1000
gccagtactc aggaatgctg gactgcgcca ggaggatcct ggccagagag 1050
ggggtggccg ccttctacaa aggtatgtc cccaacatgc tgggcatcat 1100
cccctatgcc ggcatcgacc ttgcagtcta cgagacgctc aagaatgcct 1150
ggctgcagca ctatgcagt aacagcgcgg accccggcgt gtttgtgctc 1200
ctggcctgtg gcaccatgtc cagtacctgt ggccagctgg ccagctaccc 1250
cctggcccta gtcaggacc ggatgcaggc gcaagcctct attgagggcg 1300
ctccggagggt gaccatgagc agcctcttca aacatatcct gcggaccgag 1350
ggggccttcg ggctgtacag ggggctggcc cccaacttca tgaaggatcat 1400
cccagctgtg agcatcagct acgtggtcta cgagaacctg aagatcacc 1450
tgggcgctga gtcgcggtga cggggggagg gccgcccggc agtggactcg 1500
ctgatcctgg gccgcagcct ggggtgtgca gccatctcat tctgtgaatg 1550
tgccaacact aagctgtctc gagccaagct gtgaaaacc tagacgcacc 1600
cgcagggagg gtggggagag ctggcaggcc cagggttgt cctgctgacc 1650
ccagcagacc ctctgttg ttccagcgaa gaccacaggc attccttagg 1700
gtccagggtc agcaggctcc gggctcacat gtgtaaggac aggacatttt 1750
ctgcagtgcc tgccaatagt gagcttggag cctggaggcc ggcttagttc 1800
ttccatttca cccttgagc cagctgttg ccacggcccc tgccctctgg 1850
tctgcogtgc atctccctgt gccctcttgc tgccctgctg tctgctgagg 1900
taagggtgga ggagggctac agcccacatc ccacccctc gtccaatccc 1950
ataatccatg atgaaagggt aggtcacgtg gcctcccagg cctgacttcc 2000
caacctacag cattgacgcc aacttggctg tgaaggaaga ggaaaggatc 2050
tgcccttgtg gtcactggca tctgagccct gctgatggct ggggctctcg 2100
ggcatgcttg ggagtgcagg gggctcgggc tgccctggcct ggctgcacag 2150
aaggcaagtg ctggggctca tgggtgctctg agctggcctg gaccctgtca 2200
ggatgggccc cacctcagaa ccaaaactcac tgtcccact gtggcatgag 2250
ggcagtggag caccatgttt gagggcgag ggcagagcgt ttgtgtgttc 2300
tggggaggga aggaaaagggt gttggaggcc ttaattatgg actgttggga 2350

Asp	Lys	Lys	Asn	Asp	Gly	Arg	Ile	Asp	Ala	Gln	Glu	Ile	Met	Gln	
				95					100					105	
Ser	Leu	Arg	Asp	Leu	Gly	Val	Lys	Ile	Ser	Glu	Gln	Gln	Ala	Glu	
				110					115					120	
Lys	Ile	Leu	Lys	Ser	Met	Asp	Lys	Asn	Gly	Thr	Met	Thr	Ile	Asp	
				125					130					135	
Trp	Asn	Glu	Trp	Arg	Asp	Tyr	His	Leu	Leu	His	Pro	Val	Glu	Asn	
				140					145					150	
Ile	Pro	Glu	Ile	Ile	Leu	Tyr	Trp	Lys	His	Ser	Thr	Ile	Phe	Asp	
				155					160					165	
Val	Gly	Glu	Asn	Leu	Thr	Val	Pro	Asp	Glu	Phe	Thr	Val	Glu	Glu	
				170					175					180	
Arg	Gln	Thr	Gly	Met	Trp	Trp	Arg	His	Leu	Val	Ala	Gly	Gly	Gly	
				185					190					195	
Ala	Gly	Ala	Val	Ser	Arg	Thr	Cys	Thr	Ala	Pro	Leu	Asp	Arg	Leu	
				200					205					210	
Lys	Val	Leu	Met	Gln	Val	His	Ala	Ser	Arg	Ser	Asn	Asn	Met	Gly	
				215					220					225	
Ile	Val	Gly	Gly	Phe	Thr	Gln	Met	Ile	Arg	Glu	Gly	Gly	Ala	Arg	
				230					235					240	
Ser	Leu	Trp	Arg	Gly	Asn	Gly	Ile	Asn	Val	Leu	Lys	Ile	Ala	Pro	
				245					250					255	
Glu	Ser	Ala	Ile	Lys	Phe	Met	Ala	Tyr	Glu	Gln	Ile	Lys	Arg	Leu	
				260					265					270	
Val	Gly	Ser	Asp	Gln	Glu	Thr	Leu	Arg	Ile	His	Glu	Arg	Leu	Val	
				275					280					285	
Ala	Gly	Ser	Leu	Ala	Gly	Ala	Ile	Ala	Gln	Ser	Ser	Ile	Tyr	Pro	
				290					295					300	
Met	Glu	Val	Leu	Lys	Thr	Arg	Met	Ala	Leu	Arg	Lys	Thr	Gly	Gln	
				305					310					315	
Tyr	Ser	Gly	Met	Leu	Asp	Cys	Ala	Arg	Arg	Ile	Leu	Ala	Arg	Glu	
				320					325					330	
Gly	Val	Ala	Ala	Phe	Tyr	Lys	Gly	Tyr	Val	Pro	Asn	Met	Leu	Gly	
				335					340					345	
Ile	Ile	Pro	Tyr	Ala	Gly	Ile	Asp	Leu	Ala	Val	Tyr	Glu	Thr	Leu	
				350					355					360	
Lys	Asn	Ala	Trp	Leu	Gln	His	Tyr	Ala	Val	Asn	Ser	Ala	Asp	Pro	
				365					370					375	
Gly	Val	Phe	Val	Leu	Leu	Ala	Cys	Gly	Thr	Met	Ser	Ser	Thr	Cys	
				380					385					390	
Gly	Gln	Leu	Ala	Ser	Tyr	Pro	Leu	Ala	Leu	Val	Arg	Thr	Arg	Met	
				395					400					405	

Gln	Ala	Gln	Ala	Ser	Ile	Glu	Gly	Ala	Pro	Glu	Val	Thr	Met	Ser
				410					415					420
Ser	Leu	Phe	Lys	His	Ile	Leu	Arg	Thr	Glu	Gly	Ala	Phe	Gly	Leu
				425					430					435
Tyr	Arg	Gly	Leu	Ala	Pro	Asn	Phe	Met	Lys	Val	Ile	Pro	Ala	Val
				440					445					450
Ser	Ile	Ser	Tyr	Val	Val	Tyr	Glu	Asn	Leu	Lys	Ile	Thr	Leu	Gly
				455					460					465
Val Gln Ser Arg														

<210> 290
 <211> 1658
 <212> DNA
 <213> Homo sapiens

<400> 290
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 gcatcatcat tattctggct ggagcaattg cactcatcat tggctttggt 150
 atttcagga gacactccat cacagtcact actgtcgct cagctggga 200
 cattggggag gatggaatcc tgagctgcac ttttgaacct gacatcaaac 250
 tttctgatat cgtgatacaa tggctgaagg aaggtgtttt aggcttggtc 300
 catgagttca aagaaggcaa agatgagctg tcggagcagg atgaaatggt 350
 cagaggccgg acagcagtgt ttgctgatca agtgatagtt ggcaatgcct 400
 ctttgcggt gaaaaacgtg caactcacag atgctggcac ctacaaatgt 450
 tatatcatca cttctaaagg caagggaat gctaaccttg agtataaac 500
 tggagccttc agcatgccg aagtgaatgt ggactataat gccagctcag 550
 agaccttgcg gtgtgaggct ccccgatggt tccccagcc cacagtgggtc 600
 tgggcatccc aagttgacca gggagccaac ttctcggaag tctccaatac 650
 cagctttgag ctgaactctg agaatgtgac catgaagggt gtgtctgtgc 700
 tctacaatgt tacgatcaac aacacatact cctgtatgat tgaaaatgac 750
 attgccaaag caacagggga tatcaaagt acagaatcgg agatcaaaag 800
 gcggagtcac ctacagctgc taaactcaaa ggcttctctg tgtgtctctt 850
 ctttctttgc catcagctgg gcacttctgc ctctcagccc ttacctgatg 900
 ctaaaataat gtgccttggc caaaaaaag catgcaaagt cattgttaca 950
 acagggatct acagaactat ttcaccacca gatatgacct agttttatat 1000
 ttctgggagg aaatgaattc atatctagaa gtctggagt agcaaacaag 1050

agcaagaaac aaaaagaagc caaaagcaga aggctccaat atgaacaaga 1100
 taaatctatc ttcaaagaca tattagaagt tgggaaaata attcatgtga 1150
 actagacaag tgtgttaaga gtgataagta aaatgcacgt ggagacaagt 1200
 gcatccccag atctcagggg cctccccctg cctgtcacct ggggagtgag 1250
 aggacaggat agtgcattgt ctttgtctct gaatttttag ttatatgtgc 1300
 tgtaatgttg ctctgaggaa gcccctggaa agtctatccc aacatatcca 1350
 catcttatat tccacaaatt aagctgtagt atgtacccta agacgctgct 1400
 aattgactgc cacttcgcaa ctcaggggag gctgcatttt agtaatgggt 1450
 caaatgattc actttttatg atgcttccaa aggtgccttg gcttctcttc 1500
 ccaactgaca aatgccaaag ttgagaaaaa tgatcataat tttagcataa 1550
 acagagcagt cggggacacc gattttataa ataaactgag caccttcttt 1600
 ttaaacaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1650
 aaaaaaaaa 1658

<210> 291
 <211> 282
 <212> PRT
 <213> Homo sapiens

<400> 291
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 20 25 30
 Ile Ser Gly Arg His Ser Ile Thr Val Thr Thr Val Ala Ser Ala
 35 40 45
 Gly Asn Ile Gly Glu Asp Gly Ile Leu Ser Cys Thr Phe Glu Pro
 50 55 60
 Asp Ile Lys Leu Ser Asp Ile Val Ile Gln Trp Leu Lys Glu Gly
 65 70 75
 Val Leu Gly Leu Val His Glu Phe Lys Glu Gly Lys Asp Glu Leu
 80 85 90
 Ser Glu Gln Asp Glu Met Phe Arg Gly Arg Thr Ala Val Phe Ala
 95 100 105
 Asp Gln Val Ile Val Gly Asn Ala Ser Leu Arg Leu Lys Asn Val
 110 115 120
 Gln Leu Thr Asp Ala Gly Thr Tyr Lys Cys Tyr Ile Ile Thr Ser
 125 130 135
 Lys Gly Lys Gly Asn Ala Asn Leu Glu Tyr Lys Thr Gly Ala Phe
 140 145 150
 Ser Met Pro Glu Val Asn Val Asp Tyr Asn Ala Ser Ser Glu Thr

155	160	165
Leu Arg Cys Glu Ala Pro Arg Trp Phe	Pro Gln Pro Thr Val	Val
170	175	180
Trp Ala Ser Gln Val Asp Gln Gly Ala	Asn Phe Ser Glu Val	Ser
185	190	195
Asn Thr Ser Phe Glu Leu Asn Ser Glu	Asn Val Thr Met Lys	Val
200	205	210
Val Ser Val Leu Tyr Asn Val Thr Ile	Asn Asn Thr Tyr Ser	Cys
215	220	225
Met Ile Glu Asn Asp Ile Ala Lys Ala	Thr Gly Asp Ile Lys	Val
230	235	240
Thr Glu Ser Glu Ile Lys Arg Arg Ser	His Leu Gln Leu Leu	Asn
245	250	255
Ser Lys Ala Ser Leu Cys Val Ser Ser	Phe Phe Ala Ile Ser	Trp
260	265	270
Ala Leu Leu Pro Leu Ser Pro Tyr Leu	Met Leu Lys	
275	280	

<210> 292
 <211> 1484
 <212> DNA
 <213> Homo sapiens

<400> 292
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 tgaagcgggc ctccgccggc ctgcagcggg ttcattgagcc gacctgggccc 150
 cagcagttgc tacaggagat gaagaccctc ttcttgaata ctgagtacct 200
 gatgcccttt ctctcaacc agtgtggatc cttctctat tacctcaact 250
 tggcatcgac agatctgacc ctggctgtgc ccatctgtaa ctctctggct 300
 atcatcttca cactgattgt tgggaaggcc ctgggagaag atattggtgg 350
 aaaacgtaag ttagactact gcgagtgcgg gacgcagctc tgtggatctc 400
 gacataacctg tgtagttcc ttcccagaac ccatctcccc agagtgggtg 450
 aggacacggc cttttcccat cctgcccttt cctctgcagc tgttttgctt 500
 ccttgtaggc atcagagttc cttcccctg gacagtctgg agaaagacag 550
 aggctggggt ttgggattga agaccagacc ccatctgagc cttcctcca 600
 gccctgtacc agctcctact ggcatggctg agctcagacc ctctgattt 650
 ctgcctatta tcccaggagc agttgctggc atggtgctca ccgtgatagg 700
 aatttoactc tgcatcacia gctcagttag taagaccag gggcaacagt 750
 ctaccctttg agtgggcccga acccacttcc agctctgctg cctccaggaa 800

gcccttgggc catgaagtgc tggcagtgag cggatggacc tagcacttcc 850
 cctctctggc cttagcttcc tcctctctta tggggataac agctaccta 900
 tggatcacaa taagagaaca agagtgaag agttttgtta cttcaagt 950
 ctgttcagct gcggggattt agcacaggag actctacgct caccctcagc 1000
 aacctttctg cccagcagc tctcttctg ctaacatctc aggctcccag 1050
 cccagccacc attactgtgg cctgatctgg actatcatgg tggcagggtc 1100
 catggactgc agaactccag ctgcatggaa agggccagct gcagactttg 1150
 agccagaaat gcaaacggga ggcctctggg actcagtcag agcgctttgg 1200
 ctgaatgagg ggtggaaccg agggaagaag gtgcgtcgga gtggcagatg 1250
 caggaaatga gctgtctatt agccttgcct gccccaccca tgaggtaggc 1300
 agaaatcctc actgccagcc cctcttaaag aggtagagag ctgtgagccc 1350
 cagccccacc tgactccagc acacctggcg agtagtagct gtcaataaat 1400
 ctatgtaaag agacaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1450
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1484

<210> 293
 <211> 180
 <212> PRT
 <213> Homo sapiens

<400> 293
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 20 25 30
 Gly Leu Gln Arg Val His Glu Pro Thr Trp Ala Gln Gln Leu Leu
 35 40 45
 Gln Glu Met Lys Thr Leu Phe Leu Asn Thr Glu Tyr Leu Met Pro
 50 55 60
 Phe Leu Leu Asn Gln Cys Gly Ser Leu Leu Tyr Tyr Leu Thr Leu
 65 70 75
 Ala Ser Thr Asp Leu Thr Leu Ala Val Pro Ile Cys Asn Ser Leu
 80 85 90
 Ala Ile Ile Phe Thr Leu Ile Val Gly Lys Ala Leu Gly Glu Asp
 95 100 105
 Ile Gly Gly Lys Arg Lys Leu Asp Tyr Cys Glu Cys Gly Thr Gln
 110 115 120
 Leu Cys Gly Ser Arg His Thr Cys Val Ser Ser Phe Pro Glu Pro
 125 130 135
 Ile Ser Pro Glu Trp Val Arg Thr Arg Pro Phe Pro Ile Leu Pro
 140 145 150

Phe	Pro	Leu	Gln	Leu	Phe	Cys	Phe	Leu	Val	Ala	Ile	Arg	Val	Pro
				155					160					165
Phe	Pro	Trp	Thr	Val	Trp	Arg	Lys	Thr	Glu	Ala	Gly	Val	Trp	Asp
				170					175					180

<210> 294
 <211> 1164
 <212> DNA
 <213> Homo sapiens

<400> 294
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 cggcctaaga tgccacttct tctcatgtcc caggcttgag gccctgtggt 200
 ccccatcctt gggagaagtc agctccagca ccatgaaggg catcctogtt 250
 gctggtatca ctgcagtgtg tgttgagct gtagaatctc tgagctgctg 300
 gcagtgtaat tcatgggaaa aatcctgtgt caacagcatt gcctctgaat 350
 gtccctcaca tgccaacacc agctgtatca gctcctcagc cagctcctct 400
 ctagagacac cagtcagatt ataccagaat atgttctgct cagcggagaa 450
 ctgcagtgtg gagacacaca ttacagcctt cactgtccac gtgtctgtg 500
 aagaacactt tcattttgta agccagtgtg gccaaggaaa ggaatgcagc 550
 aacaccagcg atgccctgga ccctcccctg aagaacgtgt ccagcaacgc 600
 agagtgcctt gcttggttatg aatctaattg aacttccctg cgtgggaagc 650
 cctggaaatg ctatgaagaa gaacagtgtg tctttctagt tgcagaactt 700
 aagaatgaca ttgagtctaa gagtctcgtg ctgaaaggct gttccaacgt 750
 cagtaacgcc acctgtcagt tcctgtctgg tgaaaacaag actcttgag 800
 gagtcattct tcgaaagttt gagtgtgcaa atgtaaacag cttaccccc 850
 acgtctgcac caaccacttc ccacaacgtg ggctccaaag cttccctcta 900
 cctcttggcc cttgccagcc tccttctctg gggactgctg ccctgaggtc 950
 ctggggctgc actttgcca gcacccatt tctgcttctc tgaggtccag 1000
 agcaccctt gcggtgctga caccctcttt ccctgctctg ccccgtttaa 1050
 ctgcccagta agtgggagtc acaggtctcc aggcaatgcc gacagctgcc 1100
 ttgttcttca ttattaaagc actggttcat tcaactgcaa aaaaaaaaaa 1150
 aaaaaaaaaa aaaa 1164

<210> 295
 <211> 237
 <212> PRT

<213> Homo sapiens

<400> 295

Met Lys Gly Ile Leu Val Ala Gly Ile Thr Ala Val Leu Val Ala
1 5 10 15
Ala Val Glu Ser Leu Ser Cys Val Gln Cys Asn Ser Trp Glu Lys
20 25 30
Ser Cys Val Asn Ser Ile Ala Ser Glu Cys Pro Ser His Ala Asn
35 40 45
Thr Ser Cys Ile Ser Ser Ser Ala Ser Ser Ser Leu Glu Thr Pro
50 55 60
Val Arg Leu Tyr Gln Asn Met Phe Cys Ser Ala Glu Asn Cys Ser
65 70 75
Glu Glu Thr His Ile Thr Ala Phe Thr Val His Val Ser Ala Glu
80 85 90
Glu His Phe His Phe Val Ser Gln Cys Cys Gln Gly Lys Glu Cys
95 100 105
Ser Asn Thr Ser Asp Ala Leu Asp Pro Pro Leu Lys Asn Val Ser
110 115 120
Ser Asn Ala Glu Cys Pro Ala Cys Tyr Glu Ser Asn Gly Thr Ser
125 130 135
Cys Arg Gly Lys Pro Trp Lys Cys Tyr Glu Glu Glu Gln Cys Val
140 145 150
Phe Leu Val Ala Glu Leu Lys Asn Asp Ile Glu Ser Lys Ser Leu
155 160 165
Val Leu Lys Gly Cys Ser Asn Val Ser Asn Ala Thr Cys Gln Phe
170 175 180
Leu Ser Gly Glu Asn Lys Thr Leu Gly Gly Val Ile Phe Arg Lys
185 190 195
Phe Glu Cys Ala Asn Val Asn Ser Leu Thr Pro Thr Ser Ala Pro
200 205 210
Thr Thr Ser His Asn Val Gly Ser Lys Ala Ser Leu Tyr Leu Leu
215 220 225
Ala Leu Ala Ser Leu Leu Leu Arg Gly Leu Leu Pro
230 235

<210> 296

<211> 1245

<212> DNA

<213> Homo sapiens

<400> 296

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aggtaggagg cagggttgc ctactggcc accctcccaa cccaagagc 100
ccagcccat ggtccccgcc gccggcgcgc tgctgtgggt cctgctgctg 150

65										70					75				
Arg	Leu	Ala	Gly	Pro 80	Ala	Ala	Ala	Glu	Leu 85	Leu	Ala	Ala	Thr	Val 90					
Ser	Thr	Gly	Phe	Ser 95	Arg	Ser	Ser	Ala	Ile 100	Asn	Glu	Glu	Asp	Gly 105					
Ser	Ser	Glu	Glu	Gly 110	Val	Val	Ile	Asn	Ala 115	Gly	Lys	Asp	Ser	Thr 120					
Ser	Arg	Glu	Leu	Pro 125	Ser	Ala	Thr	Pro	Asn 130	Thr	Ala	Gly	Ser	Ser 135					
Ser	Thr	Arg	Phe	Ile 140	Ala	Asn	Ser	Gln	Glu 145	Pro	Glu	Ile	Arg	Leu 150					
Thr	Ser	Ser	Leu	Pro 155	Arg	Ser	Pro	Gly	Arg 160	Ser	Thr	Glu	Asp	Leu 165					
Pro	Gly	Ser	Gln	Ala 170	Thr	Leu	Ser	Gln	Trp 175	Ser	Thr	Pro	Gly	Ser 180					
Thr	Pro	Ser	Arg	Trp 185	Pro	Ser	Pro	Ser	Pro 190	Thr	Ala	Met	Pro	Ser 195					
Pro	Glu	Asp	Leu	Arg 200	Leu	Val	Leu	Met	Pro 205	Trp	Gly	Pro	Trp	His 210					
Cys	His	Cys	Lys	Ser 215	Gly	Thr	Met	Ser	Arg 220	Ser	Arg	Ser	Gly	Lys 225					
Leu	His	Gly	Leu	Ser 230	Gly	Arg	Leu	Arg	Val 235	Gly	Ala	Leu	Ser	Gln 240					
Leu	Arg	Thr	Glu	His 245	Lys	Pro	Cys	Thr	Tyr 250	Gln	Gln	Cys	Pro	Cys 255					
Asn	Arg	Leu	Arg	Glu 260	Glu	Cys	Pro	Leu	Asp 265	Thr	Ser	Leu	Cys	Thr 270					
Asp	Thr	Asn	Cys	Ala 275	Ser	Gln	Ser	Thr	Thr 280	Ser	Thr	Arg	Thr	Thr 285					
Thr	Thr	Pro	Phe	Pro 290	Thr	Ile	His	Leu	Arg 295	Ser	Ser	Pro	Ser	Leu 300					
Pro	Pro	Ala	Ser	Pro 305	Cys	Pro	Ala	Leu	Ala 310	Phe	Trp	Lys	Arg	Val 315					
Arg	Ile	Gly	Leu	Glu 320	Asp	Ile	Trp	Asn	Ser 325	Leu	Ser	Ser	Val	Phe 330					
Thr	Glu	Met	Gln	Pro 335	Ile	Asp	Arg	Asn	Gln 340	Arg									

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<210> 298
<211> 2692
<212> DNA
<213> Homo sapiens
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<400> 298
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 tgttgtgttg cagggggtgg gtgtgttagc gtgggttagg ggaacgtgtg 1850
 tgcgcgtgct ggtgggcatg tgagatgagt gactgccggg gaatgtgtcc 1900
 acagttgaga ggttgagca ggatgaggga atcctgtcac catcaataat 1950
 cacttggtga gcgccagctc tgcccaagac gccacctggg cggacagcca 2000
 ggagctctcc atggccaggc tgcctgtgtg catgttccct gtctgggtgcc 2050
 cctttgcccg cctcctgcaa acctcacagg gtccccacac aacagtgcc 2100
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 ccagggcagg caggggccac actatgcctg tgccctggta aaggtgaccc 2400
 ctgccattta ccagcagccc tggcatgttc ctgccccaca ggaatagaat 2450
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 ggggagctat gctaggactc caacctcagg gactcgggtg gcctgcgcta 2600
 gcttcttttg atactgaaaa cttttaaggt gggaggggtg caagggatgt 2650
 gcttaataaa tcaattccaa gcctcaaaaa aaaaaaaaaa aa 2692

<210> 299
 <211> 320
 <212> PRT
 <213> Homo sapiens

<400> 299
 Met Ala Gly Leu Ala Ala Arg Leu Val Leu Leu Ala Gly Ala Ala
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 Ala Leu Ala Ser Gly Ser Gln Gly Asp Arg Glu Pro Val Tyr Arg
 20 25 30
 Asp Cys Val Leu Gln Cys Glu Glu Gln Asn Cys Ser Gly Gly Ala
 35 40 45
 Leu Asn His Phe Arg Ser Arg Gln Pro Ile Tyr Met Ser Leu Ala
 50 55 60
 Gly Trp Thr Cys Arg Asp Asp Cys Lys Tyr Glu Cys Met Trp Val
 65 70 75

Thr	Val	Gly	Leu	Tyr	Leu	Gln	Glu	Gly	His	Lys	Val	Pro	Gln	Phe	
				80					85					90	
His	Gly	Lys	Trp	Pro	Phe	Ser	Arg	Phe	Leu	Phe	Phe	Gln	Glu	Pro	
				95					100					105	
Ala	Ser	Ala	Val	Ala	Ser	Phe	Leu	Asn	Gly	Leu	Ala	Ser	Leu	Val	
				110					115					120	
Met	Leu	Cys	Arg	Tyr	Arg	Thr	Phe	Val	Pro	Ala	Ser	Ser	Pro	Met	
				125					130					135	
Tyr	His	Thr	Cys	Val	Ala	Phe	Ala	Trp	Val	Ser	Leu	Asn	Ala	Trp	
				140					145					150	
Phe	Trp	Ser	Thr	Val	Phe	His	Thr	Arg	Asp	Thr	Asp	Leu	Thr	Glu	
				155					160					165	
Lys	Met	Asp	Tyr	Phe	Cys	Ala	Ser	Thr	Val	Ile	Leu	His	Ser	Ile	
				170					175					180	
Tyr	Leu	Cys	Cys	Val	Arg	Thr	Val	Gly	Leu	Gln	His	Pro	Ala	Val	
				185					190					195	
Val	Ser	Ala	Phe	Arg	Ala	Leu	Leu	Leu	Leu	Met	Leu	Thr	Val	His	
				200					205					210	
Val	Ser	Tyr	Leu	Ser	Leu	Ile	Arg	Phe	Asp	Tyr	Gly	Tyr	Asn	Leu	
				215					220					225	
Val	Ala	Asn	Val	Ala	Ile	Gly	Leu	Val	Asn	Val	Val	Trp	Trp	Leu	
				230					235					240	
Ala	Trp	Cys	Leu	Trp	Asn	Gln	Arg	Arg	Leu	Pro	His	Val	Arg	Lys	
				245					250					255	
Cys	Val	Val	Val	Val	Leu	Leu	Leu	Gln	Gly	Leu	Ser	Leu	Leu	Glu	
				260					265					270	
Leu	Leu	Asp	Phe	Pro	Pro	Leu	Phe	Trp	Val	Leu	Asp	Ala	His	Ala	
				275					280					285	
Ile	Trp	His	Ile	Ser	Thr	Ile	Pro	Val	His	Val	Leu	Phe	Phe	Ser	
				290					295					300	
Phe	Leu	Glu	Asp	Asp	Ser	Leu	Tyr	Leu	Leu	Lys	Glu	Ser	Glu	Asp	
				305					310					315	
Lys	Phe	Lys	Leu	Asp											
				320											

<210> 300
 <211> 1674
 <212> DNA
 <213> Homo sapiens

<400> 300
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 cctctgggca tgctgcttgg gctgctgatg gccgcctgct tcaccttctg 150

cctcagtcac cagaacctga aggagtttgc cctgaccaac ccagagaaga 200
gcagcaccaa agaaacggag agaaaagaaa ccaaagccga ggaggagctg 250
gatgccgaag tcctggaggt gttccacccg acgcatgagt ggcaggccct 300
tcagccaggg caggctgtcc ctgcaggatc ccacgtacgg ctgaatcttc 350
agactgggga aagagaggca aaactccaat atgaggacaa gttccgaaat 400
aatttgaaag gcaaaaggct ggatatcaac accaacacct acacatctca 450
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gttcaaagga agacaaggca aggcaggctg aggtaaagcg gctcttccgc 550
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gctccagttt ggaagagaag attgctgcgc tctttgatct tgaatattat 700
gtccatcaga tggacaatgc gcaggacctg ctttcctttg gtggtcttca 750
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1650
aaaaaaaaaa aaaaaaaaaa aaaa 1674

<210> 301

[illegible]

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Ser His Gln Asn Leu Lys Glu Phe Ala Leu Thr Asn Pro Glu Lys
35 40 45

Ser Ser Thr Lys Glu Thr Glu Arg Lys Glu Thr Lys Ala Glu Glu
50 55 60

Glu Leu Asp Ala Glu Val Leu Glu Val Phe His Pro Thr His Glu
65 70 75

Trp Gln Ala Leu Gln Pro Gly Gln Ala Val Pro Ala Gly Ser His
80 85 90

Val Arg Leu Asn Leu Gln Thr Gly Glu Arg Glu Ala Lys Leu Gln
95 100 105

Tyr Glu Asp Lys Phe Arg Asn Asn Leu Lys Gly Lys Arg Leu Asp
110 115 120

Ile Asn Thr Asn Thr Tyr Thr Ser Gln Asp Leu Lys Ser Ala Leu
125 130 135

Ala Lys Phe Lys Glu Gly Ala Glu Met Glu Ser Ser Lys Glu Asp
140 145 150

Lys Ala Arg Gln Ala Glu Val Lys Arg Leu Phe Arg Pro Ile Glu
155 160 165

Glu Leu Lys Lys Asp Phe Asp Glu Leu Asn Val Val Ile Glu Thr
170 175 180

Asp Met Gln Ile Met Val Arg Leu Ile Asn Lys Phe Asn Ser Ser
185 190 195

Ser Ser Ser Leu Glu Glu Lys Ile Ala Ala Leu Phe Asp Leu Glu
200 205 210

Tyr Tyr Val His Gln Met Asp Asn Ala Gln Asp Leu Leu Ser Phe
215 220 225

Gly Gly Leu Gln Val Val Ile Asn Gly Leu Asn Ser Thr Glu Pro
230 235 240

Leu Val Lys Glu Tyr Ala Ala Phe Val Leu Gly Ala Ala Phe Ser
245 250 255

Ser Asn Pro Lys Val Gln Val Glu Ala Ile Glu Gly Gly Ala Leu
260 265 270

Gln Lys Leu Leu Val Ile Leu Ala Thr Glu Gln Pro Leu Thr Ala
275 280 285

Lys Lys Lys Val Leu Phe Ala Leu Cys Ser Leu Leu Arg His Phe

290	295	300
Pro Tyr Ala Gln Arg Gln Phe Leu Lys	Leu Gly Gly Leu Gln Val	
305	310	315
Leu Arg Thr Leu Val Gln Glu Lys Gly	Thr Glu Val Leu Ala Val	
320	325	330
Arg Val Val Thr Leu Leu Tyr Asp Leu	Val Thr Glu Lys Met Phe	
335	340	345
Ala Glu Glu Glu Ala Glu Leu Thr Gln	Glu Met Ser Pro Glu Lys	
350	355	360
Leu Gln Gln Tyr Arg Gln Val His Leu	Leu Pro Gly Leu Trp Glu	
365	370	375
Gln Gly Trp Cys Glu Ile Thr Ala His	Leu Leu Ala Leu Pro Glu	
380	385	390
His Asp Ala Arg Glu Lys Val Leu Gln	Thr Leu Gly Val Leu Leu	
395	400	405
Thr Thr Cys Arg Asp Arg Tyr Arg Gln	Asp Pro Gln Leu Gly Arg	
410	415	420
Thr Leu Ala Ser Leu Gln Ala Glu Tyr	Gln Val Leu Ala Ser Leu	
425	430	435
Glu Leu Gln Asp Gly Glu Asp Glu Gly	Tyr Phe Gln Glu Leu Leu	
440	445	450
Gly Ser Val Asn Ser Leu Leu Lys Glu	Leu Arg	
455	460	

<210> 302
 <211> 2136
 <212> DNA
 <213> Homo sapiens

<400> 302
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 tccattttgc ctgtcctggt caggccccca ccccccttc cacctgacca 200
 gccatggggg ctgcggtgtt tttcggtgc actttcgtcg cgttcggccc 250
 ggccttcgcg cttttcttga tcaactgtggc tggggacccg cttcgcgtta 300
 tcacctggt cgcaggggca tttttctggc tggctccct gctcctggcc 350
 tctgtggtct ggttcattt ggtccatgtg accgaccggt cagatgccc 400
 gctccagtac ggcctcctga tttttggtgc tgctgtctct gtccttctac 450
 aggaggtgtt ccgctttgcc tactacaagc tgcttaagaa ggcagatgaa 500
 gggtttagcat cgctgagtga ggacggaaga tcacccatct ccatccgcca 550

gatggcctat gtttctgggc tctccttcgg tatcatcagt ggtgtcttct 600
 ctgttatcaa tatttttggt gatgcacttg ggccaggtgt ggttgggata 650
 catggagact caccctatta cttcctgact tcagcctttc tgacagcagc 700
 cattatcctg ctccatacct tttggggagt tgtgttcttt gatgcctgtg 750
 agaggagacg gtactgggct ttgggcctgg tggttgggag tcacctactg 800
 acatcgggac tgacattcct gaacccctgg tatgaggcca gcctgctgcc 850
 catctatgca gtcactgttt ccatggggct ctgggccttc atcacagctg 900
 gagggtcctt ccgaagtatt cagcgcagcc tcttgtgtaa ggactgacta 950
 cctggactga tcgcctgaca gatcccacct gcctgtccac tgcccatgac 1000
 tgagcccagc cccagcccgg gtccattgcc cacattctct gtctccttct 1050
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 tgtgtccagg actccccctg tgtcagtgtc ctgctctcac cctgcccagg 1250
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 tocatctcca gttctggaca gtgcagggtg ccaagaaaag ggacctagtt 1450
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 ttaaccacca gcacccctcc tctccccaag gtgaagtgga gggtgctgtg 1850
 gtgagctggc cactccagag ctgcagtgcc actggaggag tcagactacc 1900
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 tgtgggaggg gcggggaggt tttctataaa ctgtatcatt ttctgctgag 2000
 ggtggagtgt cccatccttt taatcaaggt gattgtgatt ttgactaata 2050
 aaaaagaatt tgtaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2100
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 2136

<210> 303
 <211> 247
 <212> PRT
 <213> Homo sapiens

<400> 303

Met	Gly	Ala	Ala	Val	Phe	Phe	Gly	Cys	Thr	Phe	Val	Ala	Phe	Gly	
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Pro	Ala	Phe	Ala	Leu	Phe	Leu	Ile	Thr	Val	Ala	Gly	Asp	Pro	Leu	
				20					25					30	
Arg	Val	Ile	Ile	Leu	Val	Ala	Gly	Ala	Phe	Phe	Trp	Leu	Val	Ser	
				35					40					45	
Leu	Leu	Leu	Ala	Ser	Val	Val	Trp	Phe	Ile	Leu	Val	His	Val	Thr	
				50					55					60	
Asp	Arg	Ser	Asp	Ala	Arg	Leu	Gln	Tyr	Gly	Leu	Leu	Ile	Phe	Gly	
				65					70					75	
Ala	Ala	Val	Ser	Val	Leu	Leu	Gln	Glu	Val	Phe	Arg	Phe	Ala	Tyr	
				80					85					90	
Tyr	Lys	Leu	Leu	Lys	Lys	Ala	Asp	Glu	Gly	Leu	Ala	Ser	Leu	Ser	
				95					100					105	
Glu	Asp	Gly	Arg	Ser	Pro	Ile	Ser	Ile	Arg	Gln	Met	Ala	Tyr	Val	
				110					115					120	
Ser	Gly	Leu	Ser	Phe	Gly	Ile	Ile	Ser	Gly	Val	Phe	Ser	Val	Ile	
				125					130					135	
Asn	Ile	Leu	Ala	Asp	Ala	Leu	Gly	Pro	Gly	Val	Val	Gly	Ile	His	
				140					145					150	
Gly	Asp	Ser	Pro	Tyr	Tyr	Phe	Leu	Thr	Ser	Ala	Phe	Leu	Thr	Ala	
				155					160					165	
Ala	Ile	Ile	Leu	Leu	His	Thr	Phe	Trp	Gly	Val	Val	Phe	Phe	Asp	
				170					175					180	
Ala	Cys	Glu	Arg	Arg	Arg	Tyr	Trp	Ala	Leu	Gly	Leu	Val	Val	Gly	
				185					190					195	
Ser	His	Leu	Leu	Thr	Ser	Gly	Leu	Thr	Phe	Leu	Asn	Pro	Trp	Tyr	
				200					205					210	
Glu	Ala	Ser	Leu	Leu	Pro	Ile	Tyr	Ala	Val	Thr	Val	Ser	Met	Gly	
				215					220					225	
Leu	Trp	Ala	Phe	Ile	Thr	Ala	Gly	Gly	Ser	Leu	Arg	Ser	Ile	Gln	
				230					235					240	
Arg	Ser	Leu	Leu	Cys	Lys	Asp									
				245											

<210> 304
 <211> 240
 <212> DNA
 <213> Homo sapiens

<220>

<221> unsure
<222> 108, 123, 126, 154, 198, 206, 217
<223> unknown base

<400> 304
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ccttcggnat catcagtggg gtnttntctg ttatcaatat tttggctgat 150
gcanttgggc caggtgtggg tgggatccat ggagactcac cctattantt 200
cctganttca gccttntga cagcagccat tatcctgctc 240

<210> 305
<211> 378
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 58, 94, 132, 186, 191, 220, 240, 248, 280, 311, 332
<223> unknown base

<400> 305
gaccgaccgt tcagatgccg ggtccagta cggcttcctg atttttggtg 50
ctgctgtntc tgtccttcta caggaggtgt tccgctttgc ctantacaag 100
ctgcttaaga aggcagatga ggggttagca tngctgagtg aggacggaag 150
atcaccatt tccatccgcc agatggccta tgttnttggg ntttccttcg 200
gtatcatcag tgggtgtttt tctgttatca atattttggn tgatgcantt 250
gggccagggtg tgggtgggat ccatggagan tcaccctatt aattcctgaa 300
ttcagccttt ntgacagcag ccattatcct gntccatacc ttttggggag 350
ttgtgttttt tgatgcctgt gagaggag 378

<210> 306
<211> 655
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 1, 22, 129, 133, 184
<223> unknown base

<400> 306
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tccctttccc cgggggtctgg ggtgacattg cacgggcccc tcgtggggtc 100
gcgttgccac cccacgcgga ctccccagnt gngcgccct tccatttgc 150
ctgtcctggt caggccccca ccccccttcc cacntgacca gccatggggg 200
ctgcggtgtt tttcggtgc actttcgtcg cgttcggccc ggccttcgcg 250

cttttcttga tcaactgtggc tgggggacccg cttcgcgtta tcatcctgg 300
 cgagagggca tttttctggc tgggtctccct gtccttgcc tctgtggtct 350
 ggttcattctt ggtccatgtg accgaccggt cagatgccc gctccagtac 400
 ggcctcctga tttttggtgc tgctgtctct gtccttctac aggaggtgtt 450
 ccgctttgcc tactacaagc tgcttaagaa ggcagatgag gggtagcat 500
 cgctgagtga ggacggaaga taccatctt ccatccgcc gatggcctat 550
 gtttctggtc tctccttcg tatcatcagt ggtgtcttct ctgttatcaa 600
 tattttggct gatgcactt ggccaggtgt ggttgggat catggagact 650
 cacc 655

<210> 307
 <211> 650
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 52, 89, 128
 <223> unknown base

<400> 307
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 cgttgccacc ccacgcggac tcccagntg gcgcgccct cccatttgcc 150
 tgctctggtc agggcccccac ccccttccc acctgaccag ccatgggggc 200
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 tggttcatct tgggtccatgt gaccgaccgg tcagatgcc ggctccagta 400
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 tcgctgagtg aggacggaag atcaccatc tccatccgcc agatggccta 550
 tgtttctggc ctctccttcg gtatcatcag tgggtgtctt tctgttatca 600
 atattttggc tgatgcactt gggccaggtg tgggtgggat ccatggagac 650

<210> 308
 <211> 1570
 <212> DNA
 <213> Homo sapiens

<400> 308
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gctgggagca aatccccac cccctacctg ggggacaggg caagtgagac 150
ctggtgaggg tggtcagca ggcagggag gagaggtgtc tgtgcgtcct 200
gcaccacat ctttctctgt cccctccttg ccctgtctgg aggctgctag 250
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gccatggcta cagcaagacc cccctggatg tgggtgctct gtgctctgat 400
cacagccttg cttctggggg tcacagagca tgttctcgcc aacaatgatg 450
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ccacagtggc tgctcacggc cgccactgc aggaagaaag ttttcagagt 700
ccgtctcggc cactactccc tgtcaccagt ttatgaatct gggcagcaga 750
tgttccaggg ggtcaaactc atccccacc ctggctactc ccaccctggc 800
cactctaacg acctcatgct catcaaactg aacagaagaa ttctgtccac 850
taaagatgtc agaccatca acgtctctc tcattgtccc tctgctggga 900
caaagtgctt ggtgtctggc tgggggacaa ccaagagccc ccaagtgcac 950
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gtgcgaggat gcttaccga gacagataga tgacaccatg ttctgcgccg 1050
gtgacaaagc aggtagagac tcctgccagg gtgattctgg ggggcctgtg 1100
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agtggatcca ggaaaccatc caggccaact cctgagtcac ccaggactc 1250
agcacaccgg catccccacc tgctgcaggg acagccctga cactcctttc 1300
agaccctcat tccttcccag agatgttgag aatgttcac tctccagccc 1350
ctgaccccat gtctcctgga ctcaggtct gttccccca cattgggctg 1400
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gcgggggttg cgtctcaatc tcctggggc actttcatcc tcaagctcag 1500
ggcccatccc ttctctgcag ctctgaccca aatttagtcc cagaaataaa 1550
ctgagaagtg gaaaaaaaaa 1570

<210> 309

<210> 310
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 310
 tcctgtgacc acccctctaa cacc 24

<210> 311
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 311
 ctggaacatc tgctgcccag attc 24

<210> 312
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 312
 gtcggatgac agcagcagcc gcatcatcaa tggatccgac tgcgatatgc 50

<210> 313
 <211> 3010
 <212> DNA
 <213> Homo sapiens

<400> 313
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 gtgctcttcc tgaaccacgc ccacgcgccg ggcacggcgc cccacctgt 200
 cgtcagcact ggggctgcca ggcaccaacag cgccctggtc actgtggaaa 250
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<210> 314

<211> 461

<212> PRT

<213> Homo sapiens

<400> 314

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Glu	Asp	Arg	Pro	Arg	Asp	Lys	Pro	Gln	Arg	Pro	Ser	Cys	Gly	Tyr
				20					25					30
Val	Leu	Cys	Thr	Val	Leu	Leu	Ala	Leu	Ala	Val	Leu	Leu	Ala	Val
				35					40					45
Ala	Val	Thr	Gly	Ala	Val	Leu	Phe	Leu	Asn	His	Ala	His	Ala	Pro
				50					55					60
Gly	Thr	Ala	Pro	Pro	Pro	Val	Val	Ser	Thr	Gly	Ala	Ala	Ser	Ala
				65					70					75
Asn	Ser	Ala	Leu	Val	Thr	Val	Glu	Arg	Ala	Asp	Ser	Ser	His	Leu
				80					85					90
Ser	Ile	Leu	Ile	Asp	Pro	Arg	Cys	Pro	Asp	Leu	Thr	Asp	Ser	Phe
				95					100					105

Ala Arg Leu Glu Ser	Ala Gln Ala Ser	Val Leu Gln Ala Leu Thr	110	115	120
Glu His Gln Ala Gln	Pro Arg Leu Val	Gly Asp Gln Glu Gln Glu	125	130	135
Leu Leu Asp Thr Leu	Ala Asp Gln Leu	Pro Arg Leu Leu Ala Arg	140	145	150
Ala Ser Glu Leu Gln	Thr Glu Cys Met	Gly Leu Arg Lys Gly His	155	160	165
Gly Thr Leu Gly Gln	Gly Leu Ser Ala	Leu Gln Ser Glu Gln Gly	170	175	180
Arg Leu Ile Gln Leu	Leu Ser Glu Ser	Gln Gly His Met Ala His	185	190	195
Leu Val Asn Ser Val	Ser Asp Ile Leu	Asp Ala Leu Gln Arg Asp	200	205	210
Arg Gly Leu Gly Arg	Pro Arg Asn Lys	Ala Asp Leu Gln Arg Ala	215	220	225
Pro Ala Arg Gly Thr	Arg Pro Arg Gly	Cys Ala Thr Gly Ser Arg	230	235	240
Pro Arg Asp Cys Leu	Asp Val Leu Leu	Ser Gly Gln Gln Asp Asp	245	250	255
Gly Val Tyr Ser Val	Phe Pro Thr His	Tyr Pro Ala Gly Phe Gln	260	265	270
Val Tyr Cys Asp Met	Arg Thr Asp Gly	Gly Gly Trp Thr Val Phe	275	280	285
Gln Arg Arg Glu Asp	Gly Ser Val Asn	Phe Phe Arg Gly Trp Asp	290	295	300
Ala Tyr Arg Asp Gly	Phe Gly Arg Leu	Thr Gly Glu His Trp Leu	305	310	315
Gly Leu Lys Arg Ile	His Ala Leu Thr	Thr Gln Ala Ala Tyr Glu	320	325	330
Leu His Val Asp Leu	Glu Asp Phe Glu	Asn Gly Thr Ala Tyr Ala	335	340	345
Arg Tyr Gly Ser Phe	Gly Val Gly Leu	Phe Ser Val Asp Pro Glu	350	355	360
Glu Asp Gly Tyr Pro	Leu Thr Val Ala	Asp Tyr Ser Gly Thr Ala	365	370	375
Gly Asp Ser Leu Leu	Lys His Ser Gly	Met Arg Phe Thr Thr Lys	380	385	390
Asp Arg Asp Ser Asp	His Ser Glu Asn	Asn Cys Ala Ala Phe Tyr	395	400	405
Arg Gly Ala Trp Trp	Tyr Arg Asn Cys	His Thr Ser Asn Leu Asn	410	415	420

Gly Gln Tyr Leu Arg Gly Ala His Ala Ser Tyr Ala Asp Gly Val
425 430 435

Glu Trp Ser Ser Trp Thr Gly Trp Gln Tyr Ser Leu Lys Phe Ser
440 445 450

Glu Met Lys Ile Arg Pro Val Arg Glu Asp Arg
455 460

<210> 315
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 315
cacacgtcca acctcaatgg gcag 24

<210> 316
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 316
gaccagcagg gcccaaggaca agg 23

<210> 317
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 317
gttctctgag atgaagatcc ggccggtccg ggagtaccgc ttag 44

<210> 318
<211> 1841
<212> DNA
<213> Homo sapiens

<400> 318
gcagtcagag acttcccctg cccctcgctg ggaaagaaca ttaggaatgc 50
cttttagtgc cttgcttcct gaactagctc acagtagccc ggcggcccag 100
ggcaatccga ccacatttca ctctaccgc ttaggaatc cagatgcagg 150
ccaagtacag cagcagcagg gacatgctgg atgatgatgg ggacaccacc 200
atgagcctgc attctcaagc ctctgccaca actcggcatc cagagccccg 250
gogcacagag cacagggctc cctcttcaac gtggcgacca gtggccctga 300
ccctgctgac tttgtgcttg gtgctgctga tagggctggc agccctgggg 350
cttttgtttt ttcagtacta ccagctctcc aatactggtc aagacaccat 400

ttctcaaag gaagaaagat taggaaatac gtcccaagag ttgcaatctc 450
 ttcaagtcca gaatataaag cttgcaggaa gtctgcagca tgtggctgaa 500
 aaactctgtc gtgagctgta taacaaagct ggagcacaca ggtgcagccc 550
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 tctaccatgc tgaagataaa caaacaagaa gacctggaat ttgccgcgtc 700
 tcagagctac tctgagtttt tctactctta ttggacaggg cttttgcgcc 750
 ctgacagtgg caaggcctgg ctgtggatgg atggaacccc tttcacttct 800
 gaactgttcc atattataat agatgtcacc agcccaagaa gcagagactg 850
 tgtggccatc ctcaatggga tgatcttctc aaaggactgc aaagaattga 900
 agcgttgtgt ctgtgagaga agggcaggaa tggagaagcc agagagcctc 950
 catgtccccc ctgaaacatt aggcgaaggt gactgattcg ccctctgcaa 1000
 ctacaaatag cagagtgagc caggcgggtgc caaagcaagg gctagttgag 1050
 acattgggaa atggaacata atcaggaaag actatctctc tgactagtag 1100
 aaaatggggt ctctgttttc ctgttcagga tcaccagcat ttctgagctt 1150
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 caaccaacct cagaaaccca taatgtcatc tgccttcttg gcttagagat 1250
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 atgtcttctt tacacttggt ggaataagaa actttttgaa gtagaggaaa 1350
 tacattgagg taacatcctt ttctctgaca gtcaagtagt ccatcagaaa 1400
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 aatctcaaat ctcaatgcct tataagcatt ccttctctgtg tccattaaga 1600
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 actgaagatt taataataat aaatgtaaat actgtgaaaa a 1841

<210> 319
 <211> 280
 <212> PRT
 <213> Homo sapiens

<400> 319

Met Gln Ala Lys Tyr Ser Ser Thr Arg Asp Met Leu Asp Asp Asp
1 5 10 15
Gly Asp Thr Thr Met Ser Leu His Ser Gln Ala Ser Ala Thr Thr
20 25 30
Arg His Pro Glu Pro Arg Arg Thr Glu His Arg Ala Pro Ser Ser
35 40 45
Thr Trp Arg Pro Val Ala Leu Thr Leu Leu Thr Leu Cys Leu Val
50 55 60
Leu Leu Ile Gly Leu Ala Ala Leu Gly Leu Leu Phe Phe Gln Tyr
65 70 75
Tyr Gln Leu Ser Asn Thr Gly Gln Asp Thr Ile Ser Gln Met Glu
80 85 90
Glu Arg Leu Gly Asn Thr Ser Gln Glu Leu Gln Ser Leu Gln Val
95 100 105
Gln Asn Ile Lys Leu Ala Gly Ser Leu Gln His Val Ala Glu Lys
110 115 120
Leu Cys Arg Glu Leu Tyr Asn Lys Ala Gly Ala His Arg Cys Ser
125 130 135
Pro Cys Thr Glu Gln Trp Lys Trp His Gly Asp Asn Cys Tyr Gln
140 145 150
Phe Tyr Lys Asp Ser Lys Ser Trp Glu Asp Cys Lys Tyr Phe Cys
155 160 165
Leu Ser Glu Asn Ser Thr Met Leu Lys Ile Asn Lys Gln Glu Asp
170 175 180
Leu Glu Phe Ala Ala Ser Gln Ser Tyr Ser Glu Phe Phe Tyr Ser
185 190 195
Tyr Trp Thr Gly Leu Leu Arg Pro Asp Ser Gly Lys Ala Trp Leu
200 205 210
Trp Met Asp Gly Thr Pro Phe Thr Ser Glu Leu Phe His Ile Ile
215 220 225
Ile Asp Val Thr Ser Pro Arg Ser Arg Asp Cys Val Ala Ile Leu
230 235 240
Asn Gly Met Ile Phe Ser Lys Asp Cys Lys Glu Leu Lys Arg Cys
245 250 255
Val Cys Glu Arg Arg Ala Gly Met Val Lys Pro Glu Ser Leu His
260 265 270
Val Pro Pro Glu Thr Leu Gly Glu Gly Asp
275 280

<210> 320

<211> 468

<212> DNA

<213> Homo sapiens

<220>
<221> unsure
<222> 59, 95, 149, 331, 364, 438, 446
<223> unknown base

<400> 320
aattttcacc gctgtaggaa tccagatgca ggccaagtac agcagcacga 50
gggacatgnt ggatgatgat gggacaccac catgagcctg cattntcaag 100
cttttgccac aattcggcat ccagagcccc ggcgcacaga gcacagggnt 150
cctttttcaa cgtggcgacc agtggccctg accctgctga ctttgtgctt 200
gggtgctgctg atagggctgg cagccctggg gcttttgttt tttcagtact 250
accagctctc caatactggt caagacacca tttctcaaat ggaagaaaga 300
ttaggaaata cgtcccaaga gttgcaattt nttcaagtcc agaataataa 350
gcttgcagga agtntgcagc atgtggctga aaaactctgt cgtgagctgt 400
ataacaaagc tggaggaact ttgaaggagg gcaaagtntc ctcatntact 450
atacacacac cacttccc 468

<210> 321
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 321
atgcaggcca agtacagcag cac 23

<210> 322
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 322
catgctgacg acttcctgca agc 23

<210> 323
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 323
ccacacagtc totgcttott ggg 23

<210> 324
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 324
atgctggatg atgatgggga caccacatg agcctgcatt 40

<210> 325
<211> 2988
<212> DNA
<213> Homo sapiens

<400> 325
gccgagcgca agaaccctgc gcagcccaga gcagctgctg gaggggaatc 50
gaggcgcggc tccggggatt cggctcgggc cgctggctct gctctgcggg 100
gaggagcgcg gcccgcccgc ggggcccag ccctccggat cgcggccctc 150
cccgggtccc cccctcggga gactcctctg gctgctctgg gggttcgccg 200
gggcccggga cccgcgggtcc gggcgccatg cgggcatcgc tgctgctgtc 250
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ccctgagcct gctcagcgtc acctgggtgg aggagccgtg cggcccaggc 350
ccgccccaac ctggagactc tgagctgccg ccgcgcggca acaccaacgc 400
ggcgcgccgg cccaactcgg tgcagcccgg agcggagcgc gagaagcccg 450
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caccctgcac agcccggcca ggccgcaaaa aaggccgtca ggaccgccta 550
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gatccagaat accagccatc tggccgttga tggggaccgg gcagctgctt 1350
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 cacactgttc ctgctggccg ggccagacac ggtgctcacg cctgacttcc 2100
 tgaaccgctg ccgcatgcat gccatctccg gctggcaggc cttctttccc 2150
 atgcatttcc aagccttcca ccagggtgtg gcccacac aagggcctgg 2200
 gccccagag ctgggccgtg aactggccg ctttgatcgc caggcagcca 2250
 gcgaggcctg cttctacaac tccgactacg tggcagcccg tgggcgcctg 2300
 gcggcagcct cagaacaaga agaggagctg ctggagagcc tggatgtgta 2350
 cgagctgttc ctccacttct ccagtctgca tgtgctgagg gcggtggagc 2400
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 gaggacctgt accaccgctg cctccagagc gtgcttgagg gcctcggtc 2500
 ccgaaccag ctggccatgc tactctttga acaggagcag ggcaacagca 2550
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 gctgtggcct ccacgtattt atgcagtaca gtctgcctga cgcagccct 2850
 gcctctgggc cctgggggct gggctgtaga agagtgttg gggaaggagg 2900

Val Ser Ala Arg	Pro Asp Glu Trp Leu	Gly Arg Cys Ile Leu	Asp
	275	280	285
Ala Thr Gly Val	Gly Cys Thr Gly Asp	His Glu Gly Val His	Tyr
	290	295	300
Ser His Leu Glu	Leu Ser Pro Gly Glu	Pro Val Gln Glu Gly	Asp
	305	310	315
Pro His Phe Arg	Ser Ala Leu Thr Ala	His Pro Val Arg Asp	Pro
	320	325	330
Val His Met Tyr	Gln Leu His Lys Ala	Phe Ala Arg Ala Glu	Leu
	335	340	345
Glu Arg Thr Tyr	Gln Glu Ile Gln Glu	Leu Gln Trp Glu Ile	Gln
	350	355	360
Asn Thr Ser His	Leu Ala Val Asp Gly	Asp Arg Ala Ala Ala	Trp
	365	370	375
Pro Val Gly Ile	Pro Ala Pro Ser Arg	Pro Ala Ser Arg Phe	Glu
	380	385	390
Val Leu Arg Trp	Asp Tyr Phe Thr Glu	Gln His Ala Phe Ser	Cys
	395	400	405
Ala Asp Gly Ser	Pro Arg Cys Pro Leu	Arg Gly Ala Asp Arg	Ala
	410	415	420
Asp Val Ala Asp	Val Leu Gly Thr Ala	Leu Glu Glu Leu Asn	Arg
	425	430	435
Arg Tyr His Pro	Ala Leu Arg Leu Gln	Lys Gln Gln Leu Val	Asn
	440	445	450
Gly Tyr Arg Arg	Phe Asp Pro Ala Arg	Gly Met Glu Tyr Thr	Leu
	455	460	465
Asp Leu Gln Leu	Glu Ala Leu Thr Pro	Gln Gly Gly Arg Arg	Pro
	470	475	480
Leu Thr Arg Arg	Val Gln Leu Leu Arg	Pro Leu Ser Arg Val	Glu
	485	490	495
Ile Leu Pro Val	Pro Tyr Val Thr Glu	Ala Ser Arg Leu Thr	Val
	500	505	510
Leu Leu Pro Leu	Ala Ala Ala Glu Arg	Asp Leu Ala Pro Gly	Phe
	515	520	525
Leu Glu Ala Phe	Ala Thr Ala Ala Leu	Glu Pro Gly Asp Ala	Ala
	530	535	540
Ala Ala Leu Thr	Leu Leu Leu Leu Tyr	Glu Pro Arg Gln Ala	Gln
	545	550	555
Arg Val Ala His	Ala Asp Val Phe Ala	Pro Val Lys Ala His	Val
	560	565	570
Ala Glu Leu Glu	Arg Arg Phe Pro Gly	Ala Arg Val Pro Trp	Leu
	575	580	585

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 329
atggctcagt gtgcagacag 20

<210> 330
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 330
gcatgctgct ccgtgaagta gtcc 24

<210> 331
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 331
atgcatggga aagaaggcct gccc 24

<210> 332
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 332
tgcaactggtg accacgaggg ggtgcactat agccatctgg agctgag 47

<210> 333
<211> 1095
<212> DNA
<213> Homo sapiens

<400> 333
gctctggccg gccccggcga ttggtcaccg cccgctaggg gacagccctg 50
gcctcctctg attggcaagc gctggccacc tccccacacc ccttgcaaac 100
gctcccctag tggagaaaag gagtagctat tagccaattc ggcagggccc 150
gcttttttaga agcttgattt cctttgaaga tgaaagacta gcggaagctc 200
tgccctctttc ccagtgggc gagggaaactc ggggcgattg gctgggaact 250
gtatccaccc aaatgtcacc gattttcttc tatgcaggaa atgagcagac 300
ccatcaataa gaaatttctc agcctggccg aaaatggttg gccccacgaa 350
gccacgacaa ctggaggcaa agagggttgc tcaacgcccc gcctcattgg 400

aaaaccaa at cagatctggg acctatatag cgtggcggag gcggggcgat 450
gattgtcgcg ctgcaccca ctgcagctgc gcacagtcgc atttctttcc 500
ccgcccctga gaccctgcag caccatctgt catggcggct gggctgtttg 550
gtttgagcgc tcgccgtctt ttggcggcag cggcgacgcg agggctcccg 600
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cctatctgcc tgactacagg atgaaagagt ggtcccgcg cgaagctgag 900
aggcttgtga aataccgaga ggccaatggc cttcccatca tggaatccaa 950
ctgcttcgac cccagcaaga tccagctgcc agaggatgag tgaccagttg 1000
ctaagtgggg ctcaagaagc accgccttcc ccaccccctg cctgccattc 1050
tgacctcttc tcagagcacc taattaaagg ggctgaaagt ctgaa 1095

<210> 334

<211> 153

<212> PRT

<213> Homo sapiens

<400> 334

Met	Ala	Ala	Gly	Leu	Phe	Gly	Leu	Ser	Ala	Arg	Arg	Leu	Leu	Ala	1	5	10	15
Ala	Ala	Ala	Thr	Arg	Gly	Leu	Pro	Ala	Ala	Arg	Val	Arg	Trp	Glu	20	25	30	
Ser	Ser	Phe	Ser	Arg	Thr	Val	Val	Ala	Pro	Ser	Ala	Val	Ala	Gly	35	40	45	
Lys	Arg	Pro	Pro	Glu	Pro	Thr	Thr	Pro	Trp	Gln	Glu	Asp	Pro	Glu	50	55	60	
Pro	Glu	Asp	Glu	Asn	Leu	Tyr	Glu	Lys	Asn	Pro	Asp	Ser	His	Gly	65	70	75	
Tyr	Asp	Lys	Asp	Pro	Val	Leu	Asp	Val	Trp	Asn	Met	Arg	Leu	Val	80	85	90	
Phe	Phe	Phe	Gly	Val	Ser	Ile	Ile	Leu	Val	Leu	Gly	Ser	Thr	Phe	95	100	105	
Val	Ala	Tyr	Leu	Pro	Asp	Tyr	Arg	Met	Lys	Glu	Trp	Ser	Arg	Arg	110	115	120	
Glu	Ala	Glu	Arg	Leu	Val	Lys	Tyr	Arg	Glu	Ala	Asn	Gly	Leu	Pro	125	130	135	
Ile	Met	Glu	Ser	Asn	Cys	Phe	Asp	Pro	Ser	Lys	Ile	Gln	Leu	Pro	140	145	150	

[illegible]

<213> Homo sapiens

cccatcatgg aatccaactg cttcgacccc agcaagatcc ag 442

<213> Artificial Sequence

<223> Synthetic oligonucleotide probe

ctgagaccct gcagcaccat ctg 23

<213> Artificial Sequence

<223> Synthetic oligonucleotide probe

ggtgcttctt gagccccact tagc 24

<213> Artificial Sequence

<223> Synthetic oligonucleotide probe

aatctagctt ctccaggact gtggtcgccc cgtccgctgt 40

<212> DNA

[illegible]

<400> 339

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cggctggtgc	cttgcagaac	ccccacgcga	cagcctgcgg	gaggaaacttg	100
tcatcacccc	gctgccttcc	ggggacgtag	ccgccacatt	ccagttccgc	150
acgcgctggg	attcggagct	tcagcgggaa	ggagtgtccc	attacaggct	200
ctttcccaaa	gccctggggc	agctgatctc	caagtattct	ctacggggagc	250
tgcacctgtc	attcacacaa	ggcttttga	ggacccgata	ctggggggcca	300
cccttcctgc	aggccccatc	aggtgcagag	ctgtgggtct	ggttccaaga	350
cactgtcact	gatgtggata	aatcttggaa	ggagctcagt	aatgtcctct	400
cagggatctt	ctgcgcctct	ctcaacttca	tgcactccac	caacacagtc	450
actcccaactg	cctccttcaa	accctgggt	ctggccaatg	acactgacca	500
ctacttttctg	cgctatgctg	tgctgccgcg	ggaggtggtc	tgcaccgaaa	550
acctcacccc	ctggaagaag	ctcttgccct	gtagttccaa	ggcaggcctc	600
tctgtgctgc	tgaaggcaga	tcgcttgttc	cacaccagct	accactccca	650
ggcagtgcac	atccgccctg	tttgacagaaa	tgcacgctgt	actagcatct	700
cctgggagct	gaggcagacc	ctgtcagttg	tatttgatgc	cttcatcacg	750
gggcagggaa	agaaagactg	gtccctcttc	cggatgttct	cccgaaccct	800
cacggagccc	tgccccctgg	cttcagagag	ccgagtctat	gtggacatca	850
ccacctacaa	ccaggacaac	gagacattag	aggtgcaccc	acccccgacc	900
actacatatc	aggacgtcat	cctaggcact	cggaagacct	atgccatcta	950
tgacttgctt	gacaccgcca	tgatcaacaa	ctctcgaaac	ctcaacatcc	1000
agctcaagtg	gaagagaccc	ccagagaatg	agggccccc	agtgcccttc	1050
ctgcatgccc	agcgggtacgt	gagtggctat	gggctgcaga	agggggagct	1100
gagcacactg	ctgtacaaca	cccaccata	ccgggccttc	ccgggtgctgc	1150
tgctggacac	cgtaccctgg	tatctgcggc	tgtatgtgca	caccctcacc	1200
atcacctcca	agggcaagga	gaacaaacca	agttacatcc	actaccagcc	1250
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cggccaactc	agtcaccaag	gtttccatcc	agtttgagcg	ggcgctgctg	1350
aagtggaccg	agtacacgcc	agatccctaac	catggcttct	atgtcagccc	1400
atctgtcctc	agcgcccttg	tgcccagcat	ggtagcagcc	aagccagtgg	1450
actgggaaga	gagtcacctc	ttcaacagcc	tgttccagct	ctctgatggc	1500

tctaactact ttgtgctggc ctacacggag ccgctgctgg tgaacctgcc 1550
gacaccggac ttcagcatgc cctacaacgt gatctgcctc acgtgcactg 1600
tggtggccgt gtgctacggc tccttctaca atctcctcac ccgaaccttc 1650
cacatcgagg agccccgcac aggtggcctg gccaaagcggc tggccaacct 1700
tatccggcgc gcccgaggtg tccccccact ctgattcttg ccctttccag 1750
cagctgcagc tgccgtttct ctctggggag gggagcccaa gggctgtttc 1800
tgccacttgc tctcctcaga gttggctttt gaaccaaagt gccctggacc 1850
aggtcagggc ctacagctgt gttgtccagt acaggagcca cgagccaaat 1900
gtggcatttg aatttgaatt aacttagaaa ttcatttcct cacctgtagt 1950
ggccacctct atattgaggt gctcaataag caaaagtggc cggtggctgc 2000
tgtattggac agcacagaaa aagatttcca tcaccacaga aaggctcggc 2050
ggcagcactg gccaaagtga tgggggtgtg tacacagtgt atgtcactgt 2100
gtagtggatg gagtttactg tttgtggaat aaaaacggc gtttccgtgg 2150
aaaaaaaaaa aa 2162

<210> 340
<211> 574
<212> PRT
<213> Homo sapiens

<400> 340
Met Pro Leu Ala Leu Leu Val Leu Leu Leu Leu Gly Pro Gly Gly
1 5 10 15
Trp Cys Leu Ala Glu Pro Pro Arg Asp Ser Leu Arg Glu Glu Leu
20 25 30
Val Ile Thr Pro Leu Pro Ser Gly Asp Val Ala Ala Thr Phe Gln
35 40 45
Phe Arg Thr Arg Trp Asp Ser Glu Leu Gln Arg Glu Gly Val Ser
50 55 60
His Tyr Arg Leu Phe Pro Lys Ala Leu Gly Gln Leu Ile Ser Lys
65 70 75
Tyr Ser Leu Arg Glu Leu His Leu Ser Phe Thr Gln Gly Phe Trp
80 85 90
Arg Thr Arg Tyr Trp Gly Pro Pro Phe Leu Gln Ala Pro Ser Gly
95 100 105
Ala Glu Leu Trp Val Trp Phe Gln Asp Thr Val Thr Asp Val Asp
110 115 120
Lys Ser Trp Lys Glu Leu Ser Asn Val Leu Ser Gly Ile Phe Cys
125 130 135
Ala Ser Leu Asn Phe Ile Asp Ser Thr Asn Thr Val Thr Pro Thr
140 145 150

Ala Ser Phe Lys	Pro Leu Gly Leu Ala	Asn Asp Thr Asp His Tyr	155	160	165
Phe Leu Arg Tyr	Ala Val Leu Pro Arg	Glu Val Val Cys Thr Glu	170	175	180
Asn Leu Thr Pro	Trp Lys Lys Leu Leu	Pro Cys Ser Ser Lys Ala	185	190	195
Gly Leu Ser Val	Leu Leu Lys Ala Asp	Arg Leu Phe His Thr Ser	200	205	210
Tyr His Ser Gln	Ala Val His Ile Arg	Pro Val Cys Arg Asn Ala	215	220	225
Arg Cys Thr Ser	Ile Ser Trp Glu Leu	Arg Gln Thr Leu Ser Val	230	235	240
Val Phe Asp Ala	Phe Ile Thr Gly Gln	Gly Lys Lys Asp Trp Ser	245	250	255
Leu Phe Arg Met	Phe Ser Arg Thr Leu	Thr Glu Pro Cys Pro Leu	260	265	270
Ala Ser Glu Ser	Arg Val Tyr Val Asp	Ile Thr Thr Tyr Asn Gln	275	280	285
Asp Asn Glu Thr	Leu Glu Val His Pro	Pro Pro Thr Thr Thr Tyr	290	295	300
Gln Asp Val Ile	Leu Gly Thr Arg Lys	Thr Tyr Ala Ile Tyr Asp	305	310	315
Leu Leu Asp Thr	Ala Met Ile Asn Asn	Ser Arg Asn Leu Asn Ile	320	325	330
Gln Leu Lys Trp	Lys Arg Pro Pro Glu	Asn Glu Ala Pro Pro Val	335	340	345
Pro Phe Leu His	Ala Gln Arg Tyr Val	Ser Gly Tyr Gly Leu Gln	350	355	360
Lys Gly Glu Leu	Ser Thr Leu Leu Tyr	Asn Thr His Pro Tyr Arg	365	370	375
Ala Phe Pro Val	Leu Leu Leu Asp Thr	Val Pro Trp Tyr Leu Arg	380	385	390
Leu Tyr Val His	Thr Leu Thr Ile Thr	Ser Lys Gly Lys Glu Asn	395	400	405
Lys Pro Ser Tyr	Ile His Tyr Gln Pro	Ala Gln Asp Arg Leu Gln	410	415	420
Pro His Leu Leu	Glu Met Leu Ile Gln	Leu Pro Ala Asn Ser Val	425	430	435
Thr Lys Val Ser	Ile Gln Phe Glu Arg	Ala Leu Leu Lys Trp Thr	440	445	450
Glu Tyr Thr Pro	Asp Pro Asn His Gly	Phe Tyr Val Ser Pro Ser	455	460	465

Val	Leu	Ser	Ala	Leu	Val	Pro	Ser	Met	Val	Ala	Ala	Lys	Pro	Val	
				470					475					480	
Asp	Trp	Glu	Glu	Ser	Pro	Leu	Phe	Asn	Ser	Leu	Phe	Pro	Val	Ser	
				485					490					495	
Asp	Gly	Ser	Asn	Tyr	Phe	Val	Arg	Leu	Tyr	Thr	Glu	Pro	Leu	Leu	
				500					505					510	
Val	Asn	Leu	Pro	Thr	Pro	Asp	Phe	Ser	Met	Pro	Tyr	Asn	Val	Ile	
				515					520					525	
Cys	Leu	Thr	Cys	Thr	Val	Val	Ala	Val	Cys	Tyr	Gly	Ser	Phe	Tyr	
				530					535					540	
Asn	Leu	Leu	Thr	Arg	Thr	Phe	His	Ile	Glu	Glu	Pro	Arg	Thr	Gly	
				545					550					555	
Gly	Leu	Ala	Lys	Arg	Leu	Ala	Asn	Leu	Ile	Arg	Arg	Ala	Arg	Gly	
				560					565					570	

Val Pro Pro Leu

<210> 341
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 341
 tggacaccgt accctggtat ctgc 24

<210> 342
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> Artificial Sequence
 <222> 1-24
 <223> Synthetic oligonucleotide probe

<400> 342
 ccaactctga ggagagcaag tggc 24

<210> 343
 <211> 44
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 343
 tgtatgtgca caccctcacc atcacctcca agggcaagga gaac 44

<210> 344
 <211> 762
 <212> DNA
 <213> Homo sapiens

<400> 344
caacatgggg tccagcagct tcttggtcct catggtgtct ctcgttcttg 50
tgaccctggg ggctgtggaa ggagttaaag agggatataga gaaagcaggg 100
gtttgccag ctgacaacgt acgtgcttc aagtccgac cccccagtg 150
tcacacagac caggactgtc tgggggaaag gaagtgttgt tacctgcact 200
gtggcttcaa gtgtgtgatt cctgtgaagg aactggaaga aggaggaaac 250
aaggatgaag atgtgtcaag gccataccct gagccaggat gggaggccaa 300
gtgtccaggc tcctcctcta ccagggtgcc tcagaaatga tgctgggtcc 350
tttctacctc tgggggtcac tctcacttgg cacctgcccc tgagggtcct 400
gagacttgga atatggaaga agcaataccc aaccccacca aagaaaacct 450
gagcttgaag tccttttccc caaaaagagg gaagagtcac aaaaagtcca 500
gacccaggg acggtacttt ccctctctac ctggtgctcc tocctaatagc 550
tcatgaatgg acccctcatg aatgaaacca gtgcccttat aagagacccc 600
aaagagctgc cttgcccttc tgcaatgtgt gatcacagct agaaggcact 650
gtcagagaag agaaactggc cctcaccaga tgctgaatct gctgggtgcct 700
tgatcttgga cttcccagcc tctagaactg taagaaataa atatttgctg 750
tttataatcc aa 762

<210> 345
<211> 111
<212> PRT
<213> Homo sapiens

<400> 345
Met Gly Ser Ser Ser Phe Leu Val Leu Met Val Ser Leu Val Leu
1 5 10 15
Val Thr Leu Val Ala Val Glu Gly Val Lys Glu Gly Ile Glu Lys
20 25 30
Ala Gly Val Cys Pro Ala Asp Asn Val Arg Cys Phe Lys Ser Asp
35 40 45
Pro Pro Gln Cys His Thr Asp Gln Asp Cys Leu Gly Glu Arg Lys
50 55 60
Cys Cys Tyr Leu His Cys Gly Phe Lys Cys Val Ile Pro Val Lys
65 70 75
Glu Leu Glu Glu Gly Gly Asn Lys Asp Glu Asp Val Ser Arg Pro
80 85 90
Tyr Pro Glu Pro Gly Trp Glu Ala Lys Cys Pro Gly Ser Ser Ser
95 100 105
Thr Arg Cys Pro Gln Lys
110

gggaaggacg tccgctactt gcacttcctg gaaggcaccg gggactatga 1500
 gtggctggaa gcactgctta tgaatcagac ggtgatgtca aaaaaccttt 1550
 tctgggttcag gcacagaccc caggaagctt ttcgggaagc cctgcacatg 1600
 gacaggtacc tgttgctgca cccagacttt ctccgataca tgaagaacag 1650
 gtttctgagg tctaagaccc tggatggtgc cactggagg atataccgcc 1700
 ccaccactgg ggccctcctg ctgctcactg cccttcagct ctgtgaccag 1750
 gtgagtgcct atggcttcat cactgagggc catgagcgt tttctgatca 1800
 ctactatgat acatcatgga agcggctgat cttttacata aacctgact 1850
 tcaagctgga gagagaagtc tggaagcggc tacacgatga agggataatc 1900
 cggctgtacc agcgtcctgg tcccggaaact gccaaagcca agaactgacc 1950
 ggggccaggg ctgccatggc ctcttgctt gctccaaggc acaggataca 2000
 gtgggaatct tgagactctt tggccatttc ccatggctca gactaagctc 2050
 caagcccttc aggagttcca agggaaact tgaacctgga acaagactct 2100
 ctcaagatgg caaatggcta attgaggttc tgaagttctt cagtacattg 2150
 ctgtaggtcc tgaggccagg gatttttaat taaatggggg gatgggtggc 2200
 caataccaca attcctgctg aaaaacactc ttccagtcca aaagcttctt 2250
 gatacagaaa aaagagcctg gatttacaga aacatataga tctgggtttga 2300
 attccagatc gagtttacag ttgtgaaatc ttgaaggtat tacttaactt 2350
 cactacagat tgtctagaag acctttctag gagttatctg attctagaag 2400
 ggtctatact tgtccttgct tttaagctat ttgacaactc tacgtgttgt 2450
 agaaaactga taataatata aatgattgtt gtccatggaa aggcaaataa 2500
 attttctaca gtgaaaaaaaa aaaaaaaaa 2528

<210> 347
 <211> 600
 <212> PRT
 <213> Homo sapiens

<400> 347
 Met Arg Ser Cys Leu Trp Arg Cys Arg His Leu Ser Gln Gly Val
 1 5 10 15
 Gln Trp Ser Leu Leu Leu Ala Val Leu Val Phe Phe Leu Phe Ala
 20 25 30
 Leu Pro Ser Phe Ile Lys Glu Pro Gln Thr Lys Pro Ser Arg His
 35 40 45
 Gln Arg Thr Glu Asn Ile Lys Glu Arg Ser Leu Gln Ser Leu Ala
 50 55 60
 Lys Pro Lys Ser Gln Ala Pro Thr Arg Ala Arg Arg Thr Thr Ile

65										70					75				
Tyr	Ala	Glu	Pro	Ala	Pro	Glu	Asn	Asn	Ala	Leu	Asn	Thr	Gln	Thr					
				80					85					90					
Gln	Pro	Lys	Ala	His	Thr	Thr	Gly	Asp	Arg	Gly	Lys	Glu	Ala	Asn					
				95					100					105					
Gln	Ala	Pro	Pro	Glu	Glu	Gln	Asp	Lys	Val	Pro	His	Thr	Ala	Gln					
				110					115					120					
Arg	Ala	Ala	Trp	Lys	Ser	Pro	Glu	Lys	Glu	Lys	Thr	Met	Val	Asn					
				125					130					135					
Thr	Leu	Ser	Pro	Arg	Gly	Gln	Asp	Ala	Gly	Met	Ala	Ser	Gly	Arg					
				140					145					150					
Thr	Glu	Ala	Gln	Ser	Trp	Lys	Ser	Gln	Asp	Thr	Lys	Thr	Thr	Gln					
				155					160					165					
Gly	Asn	Gly	Gly	Gln	Thr	Arg	Lys	Leu	Thr	Ala	Ser	Arg	Thr	Val					
				170					175					180					
Ser	Glu	Lys	His	Gln	Gly	Lys	Ala	Ala	Thr	Thr	Ala	Lys	Thr	Leu					
				185					190					195					
Ile	Pro	Lys	Ser	Gln	His	Arg	Met	Leu	Ala	Pro	Thr	Gly	Ala	Val					
				200					205					210					
Ser	Thr	Arg	Thr	Arg	Gln	Lys	Gly	Val	Thr	Thr	Ala	Val	Ile	Pro					
				215					220					225					
Pro	Lys	Glu	Lys	Lys	Pro	Gln	Ala	Thr	Pro	Pro	Pro	Ala	Pro	Phe					
				230					235					240					
Gln	Ser	Pro	Thr	Thr	Gln	Arg	Asn	Gln	Arg	Leu	Lys	Ala	Ala	Asn					
				245					250					255					
Phe	Lys	Ser	Glu	Pro	Arg	Trp	Asp	Phe	Glu	Glu	Lys	Tyr	Ser	Phe					
				260					265					270					
Glu	Ile	Gly	Gly	Leu	Gln	Thr	Thr	Cys	Pro	Asp	Ser	Val	Lys	Ile					
				275					280					285					
Lys	Ala	Ser	Lys	Ser	Leu	Trp	Leu	Gln	Lys	Leu	Phe	Leu	Pro	Asn					
				290					295					300					
Leu	Thr	Leu	Phe	Leu	Asp	Ser	Arg	His	Phe	Asn	Gln	Ser	Glu	Trp					
				305					310					315					
Asp	Arg	Leu	Glu	His	Phe	Ala	Pro	Pro	Phe	Gly	Phe	Met	Glu	Leu					
				320					325					330					
Asn	Tyr	Ser	Leu	Val	Gln	Lys	Val	Val	Thr	Arg	Phe	Pro	Pro	Val					
				335					340					345					
Pro	Gln	Gln	Gln	Leu	Leu	Leu	Ala	Ser	Leu	Pro	Ala	Gly	Ser	Leu					
				350					355					360					
Arg	Cys	Ile	Thr	Cys	Ala	Val	Val	Gly	Asn	Gly	Gly	Ile	Leu	Asn					
				365					370					375					
Asn	Ser	His	Met	Gly	Gln	Glu	Ile	Asp	Ser	His	Asp	Tyr	Val	Phe					

	380		385		390
Arg Leu Ser Gly	Ala Leu Ile Lys Gly	Tyr Glu Gln Asp Val Gly			
	395	400			405
Thr Arg Thr Ser	Phe Tyr Gly Phe Thr	Ala Phe Ser Leu Thr Gln			
	410	415			420
Ser Leu Leu Ile	Leu Gly Asn Arg Gly	Phe Lys Asn Val Pro Leu			
	425	430			435
Gly Lys Asp Val	Arg Tyr Leu His Phe	Leu Glu Gly Thr Arg Asp			
	440	445			450
Tyr Glu Trp Leu	Glu Ala Leu Leu Met	Asn Gln Thr Val Met Ser			
	455	460			465
Lys Asn Leu Phe	Trp Phe Arg His Arg	Pro Gln Glu Ala Phe Arg			
	470	475			480
Glu Ala Leu His	Met Asp Arg Tyr Leu	Leu Leu His Pro Asp Phe			
	485	490			495
Leu Arg Tyr Met	Lys Asn Arg Phe Leu	Arg Ser Lys Thr Leu Asp			
	500	505			510
Gly Ala His Trp	Arg Ile Tyr Arg Pro	Thr Thr Gly Ala Leu Leu			
	515	520			525
Leu Leu Thr Ala	Leu Gln Leu Cys Asp	Gln Val Ser Ala Tyr Gly			
	530	535			540
Phe Ile Thr Glu	Gly His Glu Arg Phe	Ser Asp His Tyr Tyr Asp			
	545	550			555
Thr Ser Trp Lys	Arg Leu Ile Phe Tyr	Ile Asn His Asp Phe Lys			
	560	565			570
Leu Glu Arg Glu	Val Trp Lys Arg Leu	His Asp Glu Gly Ile Ile			
	575	580			585
Arg Leu Tyr Gln	Arg Pro Gly Pro Gly	Thr Ala Lys Ala Lys Asn			
	590	595			600

<210> 348
 <211> 496
 <212> DNA
 <213> Homo sapiens

<400> 348
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 gggccttcgc cggagcagcg agtggaatt gttcctcgag atctgaggat 100
 gaaggacaag tttctaaaac accttacagg cctcttttat tttagtccaa 150
 agtgcagcaa acacttccat agactttatc acâacaccag agactgcacc 200
 attcctgcat actataaaag atgcgccagg cttcttacct ggctggctgt 250
 cagtccagtg tgcatggagg ataagtgagc agaccgtaca ggagcagcac 300
 accaggagcc atgagaagtg ccttggaac caacagggaa acagaactat 350

actctaccca gctgggcccc cagtctacaa ccctgcagct cctcctccct 650
 atatgccacc acagccctct taccgggag cctgaggaac cagccatgtc 700
 tctgctgccc cttcagtgat gccaaccttg ggagatgccc tcatcctgta 750
 cctgcatctg gtcctggggg tggcaggagt cctccagcca ccaggcccca 800
 gaccaagcca agccctgggc cctactgggg acagagcccc agggaagtgg 850
 aacaggagct gaactagaac tatgaggggt tggggggagg gcttggaatt 900
 atgggctatt ttactgggg gcaagggagg gagatgacag cctgggtcac 950
 agtgccctgtt ttcaaatagt ccctctgctc ccaagatccc agccaggaag 1000
 gctggggccc tactgtttgt cccctctggg ctgggggtggg gggagggagg 1050
 aggttccgtc agcagctggc agtagccctc ctctctggct gcccactgg 1100
 ccacatctct ggctgctag attaaagctg taaagacaaa a 1141

<210> 351
 <211> 197
 <212> PRT
 <213> Homo sapiens

<400> 351
 Met Pro Pro Ala Gly Leu Arg Arg Ala Ala Pro Leu Thr Ala Ile 15
 1 5 10
 Ala Leu Leu Val Leu Gly Ala Pro Leu Val Leu Ala Gly Glu Asp 30
 20 25
 Cys Leu Trp Tyr Leu Asp Arg Asn Gly Ser Trp His Pro Gly Phe 45
 35 40
 Asn Cys Glu Phe Phe Thr Phe Cys Cys Gly Thr Cys Tyr His Arg 60
 50 55
 Tyr Cys Cys Arg Asp Leu Thr Leu Leu Ile Thr Glu Arg Gln Gln 75
 65 70
 Lys His Cys Leu Ala Phe Ser Pro Lys Thr Ile Ala Gly Ile Ala 90
 80 85
 Ser Ala Val Ile Leu Phe Val Ala Val Val Ala Thr Thr Ile Cys 105
 95 100
 Cys Phe Leu Cys Ser Cys Cys Tyr Leu Tyr Arg Arg Arg Gln Gln 120
 110 115
 Leu Gln Ser Pro Phe Glu Gly Gln Glu Ile Pro Met Thr Gly Ile 135
 125 130
 Pro Val Gln Pro Val Tyr Pro Tyr Pro Gln Asp Pro Lys Ala Gly 150
 140 145
 Pro Ala Pro Pro Gln Pro Gly Phe Met Tyr Pro Pro Ser Gly Pro 165
 155 160
 Ala Pro Gln Tyr Pro Leu Tyr Pro Ala Gly Pro Pro Val Tyr Asn 180
 170 175

CCG90440.140

Pro Ala Ala Pro Pro Pro Tyr Met Pro Pro Gln Pro Ser Tyr Pro
 185 190 195

Gly Ala

<210> 352
 <211> 3226
 <212> DNA
 <213> Homo sapiens

<400> 352
 gggggagcta ggccggcggc agtggtggtg gcgggcggcg aagggtgagg 50
 gcgggcccag aaccccaggt aggtagagca agaagatggt gtttctgccc 100
 ctcaaattgt cccttgcaac catgtcattt ctactttcct cactgttggc 150
 tctcttaact gtgtccactc cttcatgggt tcagagcact gaagcatctc 200
 caaaacgtag tgatgggaca ccatttcctt ggaataaaat acgacttcct 250
 gagtacgtca tcccagttca ttatgatctc ttgatccatg caaaccttac 300
 cacgctgacc ttctggggaa ccacgaaagt agaaatcaca gccagtcagc 350
 ccaccagcac catcatcctg catagtcacc acctgcagat atctagggcc 400
 accctcagga agggagctgg agagaggcta tcggaagaac ccctgcaggt 450
 cctggaacac cccctcagg agcaaattgc actgctggct cccgagcccc 500
 tccttgctcg gctcccgtag acagttgtca ttcactatgc tggcaatctt 550
 tcggagactt tccacggatt ttacaaaagc acctacagaa ccaaggaagg 600
 ggaactgagg atactagcat caacacaatt tgaaccact gcagctagaa 650
 tggcctttcc ctgctttgat gaacctgcct tcaaagcaag tttctcaatc 700
 aaaattagaa gagagccaag gcacctagcc atctccaata tgccattggt 750
 gaaatctgtg actgttgctg aaggactcat agaagaccat tttgatgtca 800
 ctgtgaagat gagcacctat ctggtggcct tcatcatttc agattttgag 850
 tctgtcagca agataacca gagtggagtc aaggtttctg tttatgctgt 900
 gccagacaag ataaatcaag cagattatgc actggatgct gcggtgactc 950
 ttctagaatt ttatgaggat tatttcagca taccgtatcc cctacccaaa 1000
 caagatcttg ctgctattcc cgactttcag tctggtgcta tggaaaactg 1050
 gggactgaca acatatagag aatctgctct gttgtttgat gcagaaaagt 1100
 cttctgcata aagtaagctt ggcatacag tgactgtggc ccatgaactg 1150
 gccaccagt ggtttgggaa cctggtcact atggaatggt ggaatgatct 1200
 ttggctaaat gaaggatttg ccaaatttat ggagtttgtg tctgtcagtg 1250
 tgacccatcc tgaactgaaa gttggagatt atttctttgg caaatgtttt 1300

TCCTT" 040666

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ataagggagc ttgtattctg aatatgctaa gggagtatct tagcgctgac 1450
gcatttaaaa gtggtattgt acagtatctc cagaagcata gctataaaaa 1500
tacaaaaaac gaggacctgt gggatagtat ggcaagtatt tgccctacag 1550
atgggtgtaaa agggatggat ggcttttgct ctagaagtca acattcatct 1600
tcatcctcac attggcatca ggaaggggtg gatgtgaaaa ccatgatgaa 1650
cacttggaaca ctgcagaggg gttttcccct aataaccatc acagtgaggg 1700
ggaggaatgt acacatgaag caagagcact acatgaaggg ctctgacggc 1750
gccccggaca ctgggtacct gtggcatgtt ccattgacat tcatcaccag 1800
caaatccaac atggtccatc gatttttgct aaaaacaaaa acagatgtgc 1850
tcatcctccc agaagaggtg gaatggatca aatttaaatgt gggcatgaat 1900
ggctattaca ttgtgcatta cgaggatgat ggatgggact ctttgactgg 1950
ccttttaaaa ggaacacaca cagcagtcag cagtaatgat cgggcaagtc 2000
tcattaacaa tgcatttcag ctcgctcagca ttgggaagct gtccattgaa 2050
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cgtgtttcaa ggtttgaatg agctgattcc tatgtataag ttaatggaga 2150
aaagagatat gaatgaagtg gaaactcaat tcaaggcctt cctcatcagg 2200
ctgctaaggg acctcattga taagcagaca tggacagacg agggctcagt 2250
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tgctgtgggg gccagagca cagaaggctg ggattttctt tatagtaaat 2450
atcagttttc tttgtccagt actgagaaaa gccaaattga atttgccctc 2500
tgcagaaccc aaaataagga aaagcttcaa tggctactag atgaaagctt 2550
taaggagat aaaataaaaa ctcaggagtt tccacaaatt cttacactca 2600
ttggcaggaa cccagtagga taccactgg cctggcaatt tctgaggaaa 2650
aactggaaca aacttgtaaa aaagtttgaa cttggctcat cttccatagc 2700
ccacatggta atgggtacaa caaatcaatt ctccacaaga acacggcttg 2750
aagaggtaaa aggattcttc agctctttga aagaaaatgg ttctcagctc 2800
cgttgtgtcc aacagacaat tgaaaccatt gaagaaaaca tcggttgat 2850
ggataagaat tttgataaaa tcagagtgtg gctgcaaagt gaaaagcttg 2900

215										220					225				
Thr	Val	Ala	Glu	Gly	Leu	Ile	Glu	Asp	His	Phe	Asp	Val	Thr	Val					
				230					235					240					
Lys	Met	Ser	Thr	Tyr	Leu	Val	Ala	Phe	Ile	Ile	Ser	Asp	Phe	Glu					
				245					250					255					
Ser	Val	Ser	Lys	Ile	Thr	Lys	Ser	Gly	Val	Lys	Val	Ser	Val	Tyr					
				260					265					270					
Ala	Val	Pro	Asp	Lys	Ile	Asn	Gln	Ala	Asp	Tyr	Ala	Leu	Asp	Ala					
				275					280					285					
Ala	Val	Thr	Leu	Leu	Glu	Phe	Tyr	Glu	Asp	Tyr	Phe	Ser	Ile	Pro					
				290					295					300					
Tyr	Pro	Leu	Pro	Lys	Gln	Asp	Leu	Ala	Ala	Ile	Pro	Asp	Phe	Gln					
				305					310					315					
Ser	Gly	Ala	Met	Glu	Asn	Trp	Gly	Leu	Thr	Thr	Tyr	Arg	Glu	Ser					
				320					325					330					
Ala	Leu	Leu	Phe	Asp	Ala	Glu	Lys	Ser	Ser	Ala	Ser	Ser	Lys	Leu					
				335					340					345					
Gly	Ile	Thr	Val	Thr	Val	Ala	His	Glu	Leu	Ala	His	Gln	Trp	Phe					
				350					355					360					
Gly	Asn	Leu	Val	Thr	Met	Glu	Trp	Trp	Asn	Asp	Leu	Trp	Leu	Asn					
				365					370					375					
Glu	Gly	Phe	Ala	Lys	Phe	Met	Glu	Phe	Val	Ser	Val	Ser	Val	Thr					
				380					385					390					
His	Pro	Glu	Leu	Lys	Val	Gly	Asp	Tyr	Phe	Phe	Gly	Lys	Cys	Phe					
				395					400					405					
Asp	Ala	Met	Glu	Val	Asp	Ala	Leu	Asn	Ser	Ser	His	Pro	Val	Ser					
				410					415					420					
Thr	Pro	Val	Glu	Asn	Pro	Ala	Gln	Ile	Arg	Glu	Met	Phe	Asp	Asp					
				425					430					435					
Val	Ser	Tyr	Asp	Lys	Gly	Ala	Cys	Ile	Leu	Asn	Met	Leu	Arg	Glu					
				440					445					450					
Tyr	Leu	Ser	Ala	Asp	Ala	Phe	Lys	Ser	Gly	Ile	Val	Gln	Tyr	Leu					
				455					460					465					
Gln	Lys	His	Ser	Tyr	Lys	Asn	Thr	Lys	Asn	Glu	Asp	Leu	Trp	Asp					
				470					475					480					
Ser	Met	Ala	Ser	Ile	Cys	Pro	Thr	Asp	Gly	Val	Lys	Gly	Met	Asp					
				485					490					495					
Gly	Phe	Cys	Ser	Arg	Ser	Gln	His	Ser	Ser	Ser	Ser	Ser	His	Trp					
				500					505					510					
His	Gln	Glu	Gly	Val	Asp	Val	Lys	Thr	Met	Met	Asn	Thr	Trp	Thr					
				515					520					525					
Leu	Gln	Arg	Gly	Phe	Pro	Leu	Ile	Thr	Ile	Thr	Val	Arg	Gly	Arg					

530										535					540				
Asn	Val	His	Met	Lys	Gln	Glu	His	Tyr	Met	Lys	Gly	Ser	Asp	Gly					
				545					550					555					
Ala	Pro	Asp	Thr	Gly	Tyr	Leu	Trp	His	Val	Pro	Leu	Thr	Phe	Ile					
				560					565					570					
Thr	Ser	Lys	Ser	Asn	Met	Val	His	Arg	Phe	Leu	Leu	Lys	Thr	Lys					
				575					580					585					
Thr	Asp	Val	Leu	Ile	Leu	Pro	Glu	Glu	Val	Glu	Trp	Ile	Lys	Phe					
				590					595					600					
Asn	Val	Gly	Met	Asn	Gly	Tyr	Tyr	Ile	Val	His	Tyr	Glu	Asp	Asp					
				605					610					615					
Gly	Trp	Asp	Ser	Leu	Thr	Gly	Leu	Leu	Lys	Gly	Thr	His	Thr	Ala					
				620					625					630					
Val	Ser	Ser	Asn	Asp	Arg	Ala	Ser	Leu	Ile	Asn	Asn	Ala	Phe	Gln					
				635					640					645					
Leu	Val	Ser	Ile	Gly	Lys	Leu	Ser	Ile	Glu	Lys	Ala	Leu	Asp	Leu					
				650					655					660					
Ser	Leu	Tyr	Leu	Lys	His	Glu	Thr	Glu	Ile	Met	Pro	Val	Phe	Gln					
				665					670					675					
Gly	Leu	Asn	Glu	Leu	Ile	Pro	Met	Tyr	Lys	Leu	Met	Glu	Lys	Arg					
				680					685					690					
Asp	Met	Asn	Glu	Val	Glu	Thr	Gln	Phe	Lys	Ala	Phe	Leu	Ile	Arg					
				695					700					705					
Leu	Leu	Arg	Asp	Leu	Ile	Asp	Lys	Gln	Thr	Trp	Thr	Asp	Glu	Gly					
				710					715					720					
Ser	Val	Ser	Glu	Gln	Met	Leu	Arg	Ser	Glu	Leu	Leu	Leu	Leu	Ala					
				725					730					735					
Cys	Val	His	Asn	Tyr	Gln	Pro	Cys	Val	Gln	Arg	Ala	Glu	Gly	Tyr					
				740					745					750					
Phe	Arg	Lys	Trp	Lys	Glu	Ser	Asn	Gly	Asn	Leu	Ser	Leu	Pro	Val					
				755					760					765					
Asp	Val	Thr	Leu	Ala	Val	Phe	Ala	Val	Gly	Ala	Gln	Ser	Thr	Glu					
				770					775					780					
Gly	Trp	Asp	Phe	Leu	Tyr	Ser	Lys	Tyr	Gln	Phe	Ser	Leu	Ser	Ser					
				785					790					795					
Thr	Glu	Lys	Ser	Gln	Ile	Glu	Phe	Ala	Leu	Cys	Arg	Thr	Gln	Asn					
				800					805					810					
Lys	Glu	Lys	Leu	Gln	Trp	Leu	Leu	Asp	Glu	Ser	Phe	Lys	Gly	Asp					
				815					820					825					
Lys	Ile	Lys	Thr	Gln	Glu	Phe	Pro	Gln	Ile	Leu	Thr	Leu	Ile	Gly					
				830					835					840					
Arg	Asn	Pro	Val	Gly	Tyr	Pro	Leu	Ala	Trp	Gln	Phe	Leu	Arg	Lys					

	845		850		855
Asn Trp Asn Lys Leu Val Gln Lys Phe Glu Leu Gly Ser Ser Ser	860		865		870
Ile Ala His Met Val Met Gly Thr Thr Asn Gln Phe Ser Thr Arg	875		880		885
Thr Arg Leu Glu Glu Val Lys Gly Phe Phe Ser Ser Leu Lys Glu	890		895		900
Asn Gly Ser Gln Leu Arg Cys Val Gln Gln Thr Ile Glu Thr Ile	905		910		915
Glu Glu Asn Ile Gly Trp Met Asp Lys Asn Phe Asp Lys Ile Arg	920		925		930
Val Trp Leu Gln Ser Glu Lys Leu Glu Arg Met	935		940		

<210> 354
 <211> 1587
 <212> DNA
 <213> Homo sapiens

<400> 354
 cagccacaga cgggtcatga gcgcggtatt actgctggcc ctccctggggt 50
 tcatacctccc actgccagga gtgcaggcgc tgctctgccca gtttgggaca 100
 gttcagcatg tgtggaaggt gtccgacctc ccccggaat ggacccctaa 150
 gaacaccagc tgcgacagcg gcttggggtg ccaggacacg ttgatgctca 200
 ttgagagcgg accccaagtg agcctggtgc tctccaaggg ctgcacggag 250
 gccaaaggacc aggagccccg cgtcactgag caccggatgg gccccggcct 300
 ctccctgatc tcctacacct tcgtgtgccg ccaggaggac ttctgcaaca 350
 acctcggtta ctccctcccg ctttggggcc cacagcccc agcagacca 400
 ggatccttga ggtgccaggt ctgcttgtct atggaaggct gtctggaggg 450
 gacaacagaa gagatctgcc ccaaggggac cacacactgt tatgatggcc 500
 tcctcaggct caggggagga ggcatttct ccaatctgag agtccaggga 550
 tgcattgccc agccagggtg caacctgctc aatgggacac aggaaattgg 600
 gcccgagggt atgactgaga actgcaatag gaaagatttt ctgacctgtc 650
 atcggggggac caccattatg acacacggaa acttggtctc agaaccact 700
 gattggacca catogaatac cgagatgtgc gaggtggggc aggtgtgtca 750
 ggagacgctg ctgctcatag atgtaggact cacatcaacc ctgggtgggga 800
 caaaaggctg cagcactgtt ggggctcaaa attcccagaa gaccaccatc 850
 cactcagccc ctccctggggt gcttgtggcc tcctataccc acttctgctc 900
 ctcggaacctg tgcaatagtg ccagcagcag cagcgttctg ctgaactccc 950

tccctcctca agctgcccc gtcccaggag accggcagtg tcctacctgt 1000
 gtgcagcccc ttggaacctg ttcaagtggc tccccccgaa tgacctgccc 1050
 caggggcgcc actcattgtt atgatgggta cattcatctc tcaggagggtg 1100
 ggctgtccac caaaatgagc attcagggct gcgtggccca accttccagc 1150
 ttcttgttga accacaccag acaaatcggg atcttctctg cgcgtgagaa 1200
 gcgtgatgtg cagcctcctg cctctcagca tgaggagggt ggggctgagg 1250
 gcctggagtc tctcacttgg ggggtggggc tggcactggc cccagcgctg 1300
 tgggtggggag tggtttgccc ttcctgctaa ctctattacc cccacgattc 1350
 ttcaccgctg ctgaccaccc aactcaacc tccctctgac ctcataacct 1400
 aatggccttg gacaccagat tctttcccat tctgtccatg aatcatcttc 1450
 cccacacaca atcattcata tctactcacc taacagcaac actggggaga 1500
 gcctggagca tccggacttg ccctatggga gaggggacgc tggaggagtg 1550
 gctgcatgta tctgataata cagaccctgt cctttca 1587

<210> 355
 <211> 437
 <212> PRT
 <213> Homo sapiens

<400> 355
 Met Ser Ala Val Leu Leu Ala Leu Leu Gly Phe Ile Leu Pro
 1 5 10 15
 Leu Pro Gly Val Gln Ala Leu Leu Cys Gln Phe Gly Thr Val Gln
 20 25 30
 His Val Trp Lys Val Ser Asp Leu Pro Arg Gln Trp Thr Pro Lys
 35 40 45
 Asn Thr Ser Cys Asp Ser Gly Leu Gly Cys Gln Asp Thr Leu Met
 50 55 60
 Leu Ile Glu Ser Gly Pro Gln Val Ser Leu Val Leu Ser Lys Gly
 65 70 75
 Cys Thr Glu Ala Lys Asp Gln Glu Pro Arg Val Thr Glu His Arg
 80 85 90
 Met Gly Pro Gly Leu Ser Leu Ile Ser Tyr Thr Phe Val Cys Arg
 95 100 105
 Gln Glu Asp Phe Cys Asn Asn Leu Val Asn Ser Leu Pro Leu Trp
 110 115 120
 Ala Pro Gln Pro Pro Ala Asp Pro Gly Ser Leu Arg Cys Pro Val
 125 130 135
 Cys Leu Ser Met Glu Gly Cys Leu Glu Gly Thr Thr Glu Glu Ile
 140 145 150
 Cys Pro Lys Gly Thr Thr His Cys Tyr Asp Gly Leu Leu Arg Leu

155	160	165
Arg Gly Gly Gly Ile Phe Ser Asn Leu	Arg Val Gln Gly Cys Met	
170	175	180
Pro Gln Pro Gly Cys Asn Leu Leu Asn	Gly Thr Gln Glu Ile Gly	
185	190	195
Pro Val Gly Met Thr Glu Asn Cys Asn	Arg Lys Asp Phe Leu Thr	
200	205	210
Cys His Arg Gly Thr Thr Ile Met Thr	His Gly Asn Leu Ala Gln	
215	220	225
Glu Pro Thr Asp Trp Thr Thr Ser Asn	Thr Glu Met Cys Glu Val	
230	235	240
Gly Gln Val Cys Gln Glu Thr Leu Leu	Leu Ile Asp Val Gly Leu	
245	250	255
Thr Ser Thr Leu Val Gly Thr Lys Gly	Cys Ser Thr Val Gly Ala	
260	265	270
Gln Asn Ser Gln Lys Thr Thr Ile His	Ser Ala Pro Pro Gly Val	
275	280	285
Leu Val Ala Ser Tyr Thr His Phe Cys	Ser Ser Asp Leu Cys Asn	
290	295	300
Ser Ala Ser Ser Ser Ser Val Leu Leu	Asn Ser Leu Pro Pro Gln	
305	310	315
Ala Ala Pro Val Pro Gly Asp Arg Gln	Cys Pro Thr Cys Val Gln	
320	325	330
Pro Leu Gly Thr Cys Ser Ser Gly Ser	Pro Arg Met Thr Cys Pro	
335	340	345
Arg Gly Ala Thr His Cys Tyr Asp Gly	Tyr Ile His Leu Ser Gly	
350	355	360
Gly Gly Leu Ser Thr Lys Met Ser Ile	Gln Gly Cys Val Ala Gln	
365	370	375
Pro Ser Ser Phe Leu Leu Asn His Thr	Arg Gln Ile Gly Ile Phe	
380	385	390
Ser Ala Arg Glu Lys Arg Asp Val Gln	Pro Pro Ala Ser Gln His	
395	400	405
Glu Gly Gly Gly Ala Glu Gly Leu Glu	Ser Leu Thr Trp Gly Val	
410	415	420
Gly Leu Ala Leu Ala Pro Ala Leu Trp	Trp Gly Val Val Cys Pro	
425	430	435

Ser Cys

<210> 356
 <211> 1238
 <212> DNA
 <213> Homo sapiens

<400> 356
 gcgacgggca ggacgccccg ttcgcctagc gcgtgctcag gagttggtgt 50
 cctgcctgcg ctccaggatga gggggaatct ggccctggtg ggcgttctaa 100
 tcagcctggc cttcctgtca ctgctgccat ctggacatcc tcagccggct 150
 ggcgatgacg cctgctctgt gcagatcctc gtccctggcc tcaaagggga 200
 tgccgggagag aaggggagaca aaggcgcccc cggacggcct ggaagagtcg 250
 gccccacggg agaaaaagga gacatggggg acaaaggaca gaaaggcagt 300
 gtgggtcgtc atggaaaaat tggctccatt ggctctaaag gtgagaaagg 350
 agattccggt gacataggac cccctggtcc taatggagaa ccaggcctcc 400
 catgtgagtg cagccagctg cgcaaggcca tcggggagat ggacaaccag 450
 gtctctcagc tgaccagcga gctcaagttc atcaagaatg ctgtcgccgg 500
 tgtgcgcgag acggagagca agatctacct gctggtgaag gaggagaagc 550
 gctacgcgga cggccagctg tcctgccagg gccgcggggg cagctgagc 600
 atgcccgaag acgaggtgtc caatggcctg atggccgcat acctggcgca 650
 agccggcctg gcccggtgtc tcctcgccat caacgacctg gagaaggagg 700
 gcgccttcgt gtactctgac cactccccca tgcggacctt caacaagtgg 750
 cgcagcggtg agcccaacaa tgccctacgac gaggaggact gcgtggagat 800
 ggtggcctcg ggcgggtgga acgacgtggc ctgccacacc accatgtact 850
 tcattgtgtga gtttgacaag gagaacatgt gagcctcagg ctggggctgc 900
 ccattggggg ccccatatgt ccctgcaggg ttggcaggga cagagcccag 950
 accatggtgc cagccaggga gctgtccctc tgtgaagggt ggaggctcac 1000
 tgagtagagg gctgttgtct aaactgagaa aatggcctat gcttaagagg 1050
 aaaatgaaag tgttcctggg gtgctgtctc tgaagaagca gagtttcatt 1100
 acctgtattg tagccccaat gtcattatgt aattattacc cagaattgct 1150
 cttccataaa gcttgtgcct ttgtccaagc tatacaataa aatctttaag 1200
 tagtgagta gttaagtcca aaaaaaaaaa aaaaaaaaa 1238

<210> 357
 <211> 271
 <212> PRT
 <213> Homo sapiens

<400> 357
 Met Arg Gly Asn Leu Ala Leu Val Gly Val Leu Ile Ser Leu Ala
 1 5 10 15
 Phe Leu Ser Leu Leu Pro Ser Gly His Pro Gln Pro Ala Gly Asp
 20 25 30

Asp	Ala	Cys	Ser	Val	Gln	Ile	Leu	Val	Pro	Gly	Leu	Lys	Gly	Asp		35	40	45
Ala	Gly	Glu	Lys	Gly	Asp	Lys	Gly	Ala	Pro	Gly	Arg	Pro	Gly	Arg		50	55	60
Val	Gly	Pro	Thr	Gly	Glu	Lys	Gly	Asp	Met	Gly	Asp	Lys	Gly	Gln		65	70	75
Lys	Gly	Ser	Val	Gly	Arg	His	Gly	Lys	Ile	Gly	Pro	Ile	Gly	Ser		80	85	90
Lys	Gly	Glu	Lys	Gly	Asp	Ser	Gly	Asp	Ile	Gly	Pro	Pro	Gly	Pro		95	100	105
Asn	Gly	Glu	Pro	Gly	Leu	Pro	Cys	Glu	Cys	Ser	Gln	Leu	Arg	Lys		110	115	120
Ala	Ile	Gly	Glu	Met	Asp	Asn	Gln	Val	Ser	Gln	Leu	Thr	Ser	Glu		125	130	135
Leu	Lys	Phe	Ile	Lys	Asn	Ala	Val	Ala	Gly	Val	Arg	Glu	Thr	Glu		140	145	150
Ser	Lys	Ile	Tyr	Leu	Leu	Val	Lys	Glu	Glu	Lys	Arg	Tyr	Ala	Asp		155	160	165
Ala	Gln	Leu	Ser	Cys	Gln	Gly	Arg	Gly	Gly	Thr	Leu	Ser	Met	Pro		170	175	180
Lys	Asp	Glu	Ala	Ala	Asn	Gly	Leu	Met	Ala	Ala	Tyr	Leu	Ala	Gln		185	190	195
Ala	Gly	Leu	Ala	Arg	Val	Phe	Ile	Gly	Ile	Asn	Asp	Leu	Glu	Lys		200	205	210
Glu	Gly	Ala	Phe	Val	Tyr	Ser	Asp	His	Ser	Pro	Met	Arg	Thr	Phe		215	220	225
Asn	Lys	Trp	Arg	Ser	Gly	Glu	Pro	Asn	Asn	Ala	Tyr	Asp	Glu	Glu		230	235	240
Asp	Cys	Val	Glu	Met	Val	Ala	Ser	Gly	Gly	Trp	Asn	Asp	Val	Ala		245	250	255
Cys	His	Thr	Thr	Met	Tyr	Phe	Met	Cys	Glu	Phe	Asp	Lys	Glu	Asn		260	265	270

Met

<210> 358
 <211> 972
 <212> DNA
 <213> Homo sapiens

<400> 358
 agtgactgca gccttcctag atccctcca ctcggtttct ctctttgcag 50
 gagcaccggc agcaccagtg tgtgagggga gcaggcagcg gtcctagcca 100
 gttccttgat cctgccagac caccagccc ccggcacaga gctgctccac 150

aggcaccatg aggatcatgc tgctattcac agccatcctg gccttcagcc 200
tagctcagag ctttggggct gtctgtaagg agccacagga ggaggtgggt 250
cctggcgggg gccgcagcaa gagggatcca gatctctacc agctgctcca 300
gagactcttc aaaagccact catctctgga gggattgctc aaagccctga 350
gccaggctag cacagatcct aaggaatcaa catctcccga gaaacgtgac 400
atgcatgact tctttgtggg acttatgggc aagaggagcg tccagccaga 450
gggaaagaca ggacctttct taccttcagt gagggttcct cggccccttc 500
atcccaatca gcttgatcc acaggaaagt cttccctggg aacagaggag 550
cagagacctt tataagactc tcctacggat gtgaatcaag agaacgtccc 600
cagctttggc atcctcaagt atccccgag agcagaatag gtactccact 650
tccggactcc tggactgcat taggaagacc tctttccctg tcccaatccc 700
caggtgcgca cgctcctgtt accctttctc ttcctgttc ttgtaacatt 750
cttgtgcttt gactccttct ccatcttttc tacctgaccc tgggtgtggaa 800
actgcatagt gaatatcccc aacccaatg ggcattgact gtagaatacc 850
ctagagttcc tgtagtgtcc tacattaaaa atataatgtc tctctctatt 900
cctcaacaat aaaggatttt tgcatatgaa aaaaaaaaaa aaaaaaaaaa 950
aaaaaaaaa aaaaaaaaaa aa 972

<210> 359

<211> 135

<212> PRT

<213> Homo sapiens

<400> 359

Met	Arg	Ile	Met	Leu	Leu	Phe	Thr	Ala	Ile	Leu	Ala	Phe	Ser	Leu	
1				5					10					15	
Ala	Gln	Ser	Phe	Gly	Ala	Val	Cys	Lys	Glu	Pro	Gln	Glu	Glu	Val	
				20					25					30	
Val	Pro	Gly	Gly	Gly	Arg	Ser	Lys	Arg	Asp	Pro	Asp	Leu	Tyr	Gln	
				35					40					45	
Leu	Leu	Gln	Arg	Leu	Phe	Lys	Ser	His	Ser	Ser	Leu	Glu	Gly	Leu	
				50					55					60	
Leu	Lys	Ala	Leu	Ser	Gln	Ala	Ser	Thr	Asp	Pro	Lys	Glu	Ser	Thr	
				65					70					75	
Ser	Pro	Glu	Lys	Arg	Asp	Met	His	Asp	Phe	Phe	Val	Gly	Leu	Met	
				80					85					90	
Gly	Lys	Arg	Ser	Val	Gln	Pro	Glu	Gly	Lys	Thr	Gly	Pro	Phe	Leu	
				95					100					105	
Pro	Ser	Val	Arg	Val	Pro	Arg	Pro	Leu	His	Pro	Asn	Gln	Leu	Gly	
				110					115					120	

Ser	Thr	Gly	Lys	Ser	Ser	Leu	Gly	Thr	Glu	Glu	Gln	Arg	Pro	Leu
				125					130					135

<210> 360
 <211> 1738
 <212> DNA
 <213> Homo sapiens

<400> 360
 gggcgtctcc ggctgctcct attgagctgt ctgctcgctg tgcccgtgt 50
 gcctgctgtg cccgcgctgt cgccgctgct accgcgtctg ctggacgcgg 100
 gagacgccag cgagctggtg attggagccc tgcggagagc tcaagcggcc 150
 agctctgccc caggagccca ggctgccccg tgagtcccat agttgctgca 200
 ggagtggagc catgagctgc gtctgggtg gtgtcatccc cttggggctg 250
 ctgttctctg tctgcggatc ccaaggctac ctctgcccc acgtcactct 300
 cttagaggag ctgctcagca aataccagca caacgagtct cactcccggg 350
 tccgcagagc catccccagg gaggacaagg aggagatcct catgctgcac 400
 aacaagcttc ggggccaggt gcagcctcag gcctccaaca tggagtacat 450
 ggtgagcgcc ggctccggcc gcagaggctg gcaccggggg tggggcctgg 500
 gccaccagcc tgctctgttc ccagccagc tctgttcccc agccagtgcg 550
 tgtgatggct ggctcagggt ctctctggc aggggaggat cccggctctg 600
 ttctgttttg tttgtttgtt ttgagacagg gtctcactct gccactgacg 650
 ctggagtgca atggcacaat cgtcatgccc tgaaacctta gactcccggg 700
 gttaagcgat cctgcttcag cctcccaagt agctggaact acaggcatgc 750
 accatggtgc ccagctagat tttaaatatt ttgtggagat gggggctctg 800
 ctacgttgcc caggctggtc ttgaactcct aggtcaagc aatcctcctg 850
 cctcagcctc tcaaagtgtc aggattatag gcatgagtca ccctgtctgg 900
 ctctggctct gttcttaaca ttctgcaaaa acaacacacg tgggttccct 950
 gtgcagagcc tgctcgttg cttcatgtc actcttggtg gctccactgg 1000
 gaacacagct ctcagccttt ccacctgga ggcagagtgg ggaggggccc 1050
 agggtgggc tttgctgatg ctgatctcag ctgtgccaca cgctagctgc 1100
 accaccctga cttctcctta gcccggtgta gcctcacttt ccacttgag 1150
 agtcttctc cgcgtgggtg ccatgactgt gagataagtc gaggtgtgta 1200
 agggcccggc acagactgac ctgcctcccc aaccctagg ctttgctaac 1250
 cgggaaagga gctaacggtg acagaagaca gccaaagtca accctcccgg 1300
 gtgattgtga tgggtgttcc aggtgtggtt gggcgatgct gctacttgac 1350

cccaagctcc agtgtggaaa cttccttcct ggctgggttt ccagaactac 1400
 agaggaatgg accacagtct tccaggggtcc ctctcgtcc accaaccggg 1450
 agcctccacc ttggccatcc gtcagctatg aatggctttt taaacaaacc 1500
 cacgtcccag cctgggtaac atggtaaagc cccgtctcta caaaaaaatc 1550
 caagttagcc gggcatgggtg gtgcgcacct gtagtcccag ctgcagtggg 1600
 actgaggtgg aggtggaggt ggggggtggg agctgaggaa ggaggatcgc 1650
 ttgagcctgg gaagtcgagg ctgcagtgag ctgagattgc accactgcac 1700
 tccagcctgg gtgacagagc aagaccctgt ctcaaaaa 1738

<210> 361
 <211> 159
 <212> PRT
 <213> Homo sapiens

<400> 361
 Met Ser Cys Val Leu Gly Gly Val Ile Pro Leu Gly Leu Leu Phe
 1 5 10 15
 Leu Val Cys Gly Ser Gln Gly Tyr Leu Leu Pro Asn Val Thr Leu
 20 25 30
 Leu Glu Glu Leu Leu Ser Lys Tyr Gln His Asn Glu Ser His Ser
 35 40 45
 Arg Val Arg Arg Ala Ile Pro Arg Glu Asp Lys Glu Glu Ile Leu
 50 55 60
 Met Leu His Asn Lys Leu Arg Gly Gln Val Gln Pro Gln Ala Ser
 65 70 75
 Asn Met Glu Tyr Met Val Ser Ala Gly Ser Gly Arg Arg Gly Trp
 80 85 90
 His Arg Gly Trp Gly Leu Gly His Gln Pro Ala Leu Phe Pro Ser
 95 100 105
 Gln Leu Cys Ser Pro Ala Ser Ala Cys Asp Gly Trp Leu Arg Val
 110 115 120
 Ser Ser Gly Arg Gly Gly Ser Arg Leu Cys Ser Val Leu Phe Val
 125 130 135
 Cys Phe Glu Thr Gly Ser His Ser Ala Thr Asp Ala Gly Val Gln
 140 145 150
 Trp His Asn Arg His Ala Leu Lys Pro
 155

<210> 362
 <211> 422
 <212> DNA
 <213> Homo sapiens

<400> 362
 aaggagaggc caccgggact tcagtgtctc ctccatccca ggagcgcagt 50

ggccactatg gggctctgggc tgccccttgt cctcctcttg accctccttg 100
 gcagctcaca tggaacaggg ccgggtatga ctttgcaact gaagctgaag 150
 gagtcttttc tgacaaattc ctcttatgag tccagcttcc tggaattgct 200
 tgaaaagctc tgcctcctcc tccatctccc ttcagggacc agcgtcacc 250
 tccacatgc aagatctcaa caccatgttg tctgcaacac atgacagcca 300
 ttgaagcctg tgtccttctt ggcccgggct tttgggcccgg ggatgcagga 350
 ggcaggcccc gaccctgtct ttcagcaggc cccaccctc ctgagtggca 400
 ataaataaaa ttcggtatgc tg 422

<210> 363
 <211> 78
 <212> PRT
 <213> Homo sapiens

<400> 363
 Met Gly Ser Gly Leu Pro Leu Val Leu Leu Leu Thr Leu Leu Gly
 1 5 10 15
 Ser Ser His Gly Thr Gly Pro Gly Met Thr Leu Gln Leu Lys Leu
 20 25 30
 Lys Glu Ser Phe Leu Thr Asn Ser Ser Tyr Glu Ser Ser Phe Leu
 35 40 45
 Glu Leu Leu Glu Lys Leu Cys Leu Leu Leu His Leu Pro Ser Gly
 50 55 60
 Thr Ser Val Thr Leu His His Ala Arg Ser Gln His His Val Val
 65 70 75

Cys Asn Thr

<210> 364
 <211> 826
 <212> DNA
 <213> Homo sapiens

<400> 364
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 ctttctgagt ttcaaaaaca acagactagt actctaaaga actctttaaa 100
 acaattaact gttaggattg cagttatgat tggatattat ttaattctgt 150
 ttctgatgtg gggttcctcc actgtgttct gtgtgctatt aatatttacc 200
 attgcagaag cttcattcag tggtgaaaat gaatgcttag tggatctgtg 250
 cctcttacgc atatgttaca aattatctgg agttcctaata caatgcagag 300
 ttcccctccc ctccgattgt tctaaataat tgaaagatgt ctgctgtgga 350
 aaaaggcatg tatttaaatc tgtatgattc tcaaccatct ttagttggga 400
 aaggctcctg aaagccaatg gaaatacttt ttttttttct tggcactaat 450

caagtgagtg ttaccttttc acttagtagg atgtgttggt acgctagtaa 500
aatagaaacc tgtgtttatt ctcagggtatt ttagaaacaa cagccatcat 550
tttattttat gtgtgtgttc ttggctgtat tcataaatta tatattttgg 600
gctatcaaatt attacttcat tcaatataaa taacaatagt agaagttggt 650
tacttagata tgctttctag ttgcattttc tcagcctatg taagactact 700
ttgttgtaat agcctttgaa atttacagta ctgtctctct actatcttca 750
gattacttga ttcaaataaa ccaattatgt ttgtaattga tattaataaa 800
accagaataa aagttcatat ctaccc 826

<210> 365
<211> 67
<212> PRT
<213> Homo sapiens

<400> 365
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1 5 10 15
Thr Val Phe Cys Val Leu Leu Ile Phe Thr Ile Ala Glu Ala Ser
20 25 30
Phe Ser Val Glu Asn Glu Cys Leu Val Asp Leu Cys Leu Leu Arg
35 40 45
Ile Cys Tyr Lys Leu Ser Gly Val Pro Asn Gln Cys Arg Val Pro
50 55 60
Leu Pro Ser Asp Cys Ser Lys
65

<210> 366
<211> 2475
<212> DNA
<213> Homo sapiens

<400> 366
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gttccttgca gcttttctgc ccccgccgca gtgtaccag gacccagcca 200
tggtgcatta catctaccag cgctttcgag tcttggagca agggctggaa 250
aaatgtaccc aagcaacgag ggcatacatt caagaattcc aagagttctc 300
aaaaaatata tctgtcatgc tgggaagatg tcagacctac acaagtgagt 350
acaagagtgc agtgggtaac ttggcactga gagttgaacg tgcccaacgg 400
gagattgact acatacaata ccttcgagag gctgacgagt gcatcgatatc 450
agaggacaag aactggcag aaatgttgct ccaagaagct gaagaagaga 500

aaaagatccg gactctgctg aatgcaagct gtgacaacat gctgatgggc 550
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 gatgaaagat gctgtctata actctccaaa ggtgtactta ttaattggat 650
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 acagtactgg gggccagggc cctcatcgca tcacctgcat ctatgatcca 1150
 ctgggcacta tcagtgagga ggacttgccc aacttggttct tccccagag 1200
 accaagaagt cactccatga tccattacaa cccagagat aagcagctct 1250
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 aagctgcctc tgaagtaatg cattacagct gtgagaaaga gcactgtggc 1350
 tttggcagct gttctacagg acagtgaggc tatagcccct tcacaatata 1400
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 tgagagcata tcatcaggaa agtttcaaca atgtccatta ctccccaaa 1550
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 tgggattaca ggcatgtgcc accacacctg gcttaaaata ctatttctta 1950
 ttgaggttta acctctattt ccctagccc tgtccttcca ctaagcttgg 2000
 tagatgtaat aataaagtga aaatattaac atttgaatat cgctttccag 2050
 gtgtggagtg tttgcacatc attgaattct cgtttcacct ttgtgaaaca 2100

tgcacaagtc ttacagctg tcattctaga gtttaggtga gtaacacaat 2150
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 cattgcccaa ggaagcatca aatacgtatg ttgttcacc tactottata 2250
 gtcaatgcgt tcatcgtttc agcctaaaaa taatagtctg tcccttttagc 2300
 cagttttcat gtctgcacaa gacctttcaa taggcctttc aaatgataat 2350
 tcctccagaa aaccagtcta agggtagga cccaactct agcctcctct 2400
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<210> 367
 <211> 402
 <212> PRT
 <213> Homo sapiens

<400> 367
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 20 25 30
 Met Val His Tyr Ile Tyr Gln Arg Phe Arg Val Leu Glu Gln Gly
 35 40 45
 Leu Glu Lys Cys Thr Gln Ala Thr Arg Ala Tyr Ile Gln Glu Phe
 50 55 60
 Gln Glu Phe Ser Lys Asn Ile Ser Val Met Leu Gly Arg Cys Gln
 65 70 75
 Thr Tyr Thr Ser Glu Tyr Lys Ser Ala Val Gly Asn Leu Ala Leu
 80 85 90
 Arg Val Glu Arg Ala Gln Arg Glu Ile Asp Tyr Ile Gln Tyr Leu
 95 100 105
 Arg Glu Ala Asp Glu Cys Ile Val Ser Glu Asp Lys Thr Leu Ala
 110 115 120
 Glu Met Leu Leu Gln Glu Ala Glu Glu Glu Lys Lys Ile Arg Thr
 125 130 135
 Leu Leu Asn Ala Ser Cys Asp Asn Met Leu Met Gly Ile Lys Ser
 140 145 150
 Leu Lys Ile Val Lys Lys Met Met Asp Thr His Gly Ser Trp Met
 155 160 165
 Lys Asp Ala Val Tyr Asn Ser Pro Lys Val Tyr Leu Leu Ile Gly
 170 175 180
 Ser Arg Asn Asn Thr Val Trp Glu Phe Ala Asn Ile Arg Ala Phe
 185 190 195
 Met Glu Asp Asn Thr Lys Pro Ala Pro Arg Lys Gln Ile Leu Thr
 200 205 210

Leu	Ser	Trp	Gln	Gly	Thr	Gly	Gln	Val	Ile	Tyr	Lys	Gly	Phe	Leu
				215					220					225
Phe	Phe	His	Asn	Gln	Ala	Thr	Ser	Asn	Glu	Ile	Ile	Lys	Tyr	Asn
				230					235					240
Leu	Gln	Lys	Arg	Thr	Val	Glu	Asp	Arg	Met	Leu	Leu	Pro	Gly	Gly
				245					250					255
Val	Gly	Arg	Ala	Leu	Val	Tyr	Gln	His	Ser	Pro	Ser	Thr	Tyr	Ile
				260					265					270
Asp	Leu	Ala	Val	Asp	Glu	His	Gly	Leu	Trp	Ala	Ile	His	Ser	Gly
				275					280					285
Pro	Gly	Thr	His	Ser	His	Leu	Val	Leu	Thr	Lys	Ile	Glu	Pro	Gly
				290					295					300
Thr	Leu	Gly	Val	Glu	His	Ser	Trp	Asp	Thr	Pro	Cys	Arg	Ser	Gln
				305					310					315
Asp	Ala	Glu	Ala	Ser	Phe	Leu	Leu	Cys	Gly	Val	Leu	Tyr	Val	Val
				320					325					330
Tyr	Ser	Thr	Gly	Gly	Gln	Gly	Pro	His	Arg	Ile	Thr	Cys	Ile	Tyr
				335					340					345
Asp	Pro	Leu	Gly	Thr	Ile	Ser	Glu	Glu	Asp	Leu	Pro	Asn	Leu	Phe
				350					355					360
Phe	Pro	Lys	Arg	Pro	Arg	Ser	His	Ser	Met	Ile	His	Tyr	Asn	Pro
				365					370					375
Arg	Asp	Lys	Gln	Leu	Tyr	Ala	Trp	Asn	Glu	Gly	Asn	Gln	Ile	Ile
				380					385					390
Tyr	Lys	Leu	Gln	Thr	Lys	Arg	Lys	Leu	Pro	Leu	Lys			
				395					400					

<210> 368
 <211> 2281
 <212> DNA
 <213> Homo sapiens

<400> 368
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 ctggccctga tggcgacggc ggcggtagcg cgggggtggc tgcgcgcggg 150
 ggaggagagg agcggccggc ccgcctgccaaaagcaaat ggatttccac 200
 ctgacaaatc ttcgggatcc aagaagcaga aacaatatca gcggattcgg 250
 aaggagaagc ctcaacaaca caacttcacc caccgcctcc tggctgcagc 300
 tctgaagagc cacagcggga acatatcttg catggacttt agcagcaatg 350
 gcaaatacct ggctacctgt gcagatgac gcacatccg catctggagc 400
 accaaggact tcctgcagcg agagcaccgc agcatgagag ccaacgtgga 450

gctggaccac gccaccctgg tgcgcttcag ccctgactgc agagccttca 500
tcgtctggct ggccaacggg gacaccctcc gtgtcttcaa gatgaccaag 550
cgggaggatg ggggctacac cttcacagcc accccagagg acttccctaa 600
aaagcacaag ggcctgtca tcgacattgg cattgctaac acagggaagt 650
ttatcatgac tgcctccagt gacaccactg tcctcatctg gagcctgaag 700
ggtcaagtgc tgtctaccat caacaccaac cagatgaaca acacacacgc 750
tgctgtatct ccctgtggca gatttgtagc ctctgtgtggc ttcaccccag 800
atgtgaaggt ttgggaagtc tgctttggaa agaaggggga gttccaggag 850
gtggtgcgag ccttcgaact aaagggccac tccgcggctg tgcactcgtt 900
tgctttctcc aacgactcac ggaggatggc ttctgtctcc aaggatggta 950
catggaaact gtgggacaca gatgtggaat acaagaagaa gcaggacccc 1000
taattgtga agacaggccg ctttgaagag gcggcggtg ccgcgccgtg 1050
ccgcctggcc ctctcccca acgcccaggt cttggccttg gccagtggca 1100
gtagtattca tctctacaat acccggcggg gcgagaagga ggagtgcttt 1150
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gcctccaacg agagcaccg ccagaggctg cagcagcagc tgaccacaggc 1350
ccaagagacc ctgaagagcc tgggtgccct gaagaagtga ctctgggagg 1400
gcccggcgca gaggattgag gaggagggat ctggcctcct catggcactg 1450
ctgccatctt tcctcccagg tggaagcctt tcagaaggag tctcctgggt 1500
ttcttactgg tggccctgct tcttcccatt gaaactactc ttgtctactt 1550
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tggccttggt gcagcacatc ctcacacca aagaagtttg taaatgttcc 1750
agaacaacct agagaacacc tgagtactaa gcagcagttt tgcaaggatg 1800
ggagactggg atagcttccc atcacagaac tgtgttccat caaaaagaca 1850
ctaagggatt tccttctggg cctcagttct atttgtaaga tggagaataa 1900
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gtcatgaaag tggtaaaagt gggaaccagt gtgctttgaa accaaattag 2050

aaacacattc cttggaagg caaagttttc tgggacttga tcatacattt 2100
 tatatggttg ggactttctc cttcgggaga tgatatcttg ttttaaggaga 2150
 cctctttttca gttcatcaag ttcacagat atttgagtgc ccactctgtg 2200
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa a 2281

<210> 369
 <211> 447
 <212> PRT
 <213> Homo sapiens

<400> 369

Met	Glu	Leu	Ser	Gln	Met	Ser	Glu	Leu	Met	Gly	Leu	Ser	Val	Leu	
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Leu	Gly	Leu	Leu	Ala	Leu	Met	Ala	Thr	Ala	Ala	Val	Ala	Arg	Gly	
				20					25					30	
Trp	Leu	Arg	Ala	Gly	Glu	Glu	Arg	Ser	Gly	Arg	Pro	Ala	Cys	Gln	
				35					40					45	
Lys	Ala	Asn	Gly	Phe	Pro	Pro	Asp	Lys	Ser	Ser	Gly	Ser	Lys	Lys	
				50					55					60	
Gln	Lys	Gln	Tyr	Gln	Arg	Ile	Arg	Lys	Glu	Lys	Pro	Gln	Gln	His	
				65					70					75	
Asn	Phe	Thr	His	Arg	Leu	Leu	Ala	Ala	Ala	Leu	Lys	Ser	His	Ser	
				80					85					90	
Gly	Asn	Ile	Ser	Cys	Met	Asp	Phe	Ser	Ser	Asn	Gly	Lys	Tyr	Leu	
				95					100					105	
Ala	Thr	Cys	Ala	Asp	Asp	Arg	Thr	Ile	Arg	Ile	Trp	Ser	Thr	Lys	
				110					115					120	
Asp	Phe	Leu	Gln	Arg	Glu	His	Arg	Ser	Met	Arg	Ala	Asn	Val	Glu	
				125					130					135	
Leu	Asp	His	Ala	Thr	Leu	Val	Arg	Phe	Ser	Pro	Asp	Cys	Arg	Ala	
				140					145					150	
Phe	Ile	Val	Trp	Leu	Ala	Asn	Gly	Asp	Thr	Leu	Arg	Val	Phe	Lys	
				155					160					165	
Met	Thr	Lys	Arg	Glu	Asp	Gly	Gly	Tyr	Thr	Phe	Thr	Ala	Thr	Pro	
				170					175					180	
Glu	Asp	Phe	Pro	Lys	Lys	His	Lys	Ala	Pro	Val	Ile	Asp	Ile	Gly	
				185					190					195	
Ile	Ala	Asn	Thr	Gly	Lys	Phe	Ile	Met	Thr	Ala	Ser	Ser	Asp	Thr	
				200					205					210	
Thr	Val	Leu	Ile	Trp	Ser	Leu	Lys	Gly	Gln	Val	Leu	Ser	Thr	Ile	
				215					220					225	
Asn	Thr	Asn	Gln	Met	Asn	Asn	Thr	His	Ala	Ala	Val	Ser	Pro	Cys	
				230					235					240	

Gly	Arg	Phe	Val	Ala	Ser	Cys	Gly	Phe	Thr	Pro	Asp	Val	Lys	Val	245	250	255
Trp	Glu	Val	Cys	Phe	Gly	Lys	Lys	Gly	Glu	Phe	Gln	Glu	Val	Val	260	265	270
Arg	Ala	Phe	Glu	Leu	Lys	Gly	His	Ser	Ala	Ala	Val	His	Ser	Phe	275	280	285
Ala	Phe	Ser	Asn	Asp	Ser	Arg	Arg	Met	Ala	Ser	Val	Ser	Lys	Asp	290	295	300
Gly	Thr	Trp	Lys	Leu	Trp	Asp	Thr	Asp	Val	Glu	Tyr	Lys	Lys	Lys	305	310	315
Gln	Asp	Pro	Tyr	Leu	Leu	Lys	Thr	Gly	Arg	Phe	Glu	Glu	Ala	Ala	320	325	330
Gly	Ala	Ala	Pro	Cys	Arg	Leu	Ala	Leu	Ser	Pro	Asn	Ala	Gln	Val	335	340	345
Leu	Ala	Leu	Ala	Ser	Gly	Ser	Ser	Ile	His	Leu	Tyr	Asn	Thr	Arg	350	355	360
Arg	Gly	Glu	Lys	Glu	Glu	Cys	Phe	Glu	Arg	Val	His	Gly	Glu	Cys	365	370	375
Ile	Ala	Asn	Leu	Ser	Phe	Asp	Ile	Thr	Gly	Arg	Phe	Leu	Ala	Ser	380	385	390
Cys	Gly	Asp	Arg	Ala	Val	Arg	Leu	Phe	His	Asn	Thr	Pro	Gly	His	395	400	405
Arg	Ala	Met	Val	Glu	Glu	Met	Gln	Gly	His	Leu	Lys	Arg	Ala	Ser	410	415	420
Asn	Glu	Ser	Thr	Arg	Gln	Arg	Leu	Gln	Gln	Gln	Leu	Thr	Gln	Ala	425	430	435
Gln	Glu	Thr	Leu	Lys	Ser	Leu	Gly	Ala	Leu	Lys	Lys				440	445	

<210> 370
 <211> 1415
 <212> DNA
 <213> Homo sapiens

<400> 370
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 ccacgcgagt ctcaatcatg ctctcctag taactgtgtc tgactgtgct 150
 gtgatcacag gggcctgtga gcgggatgtc cagtgtgggg caggcacctg 200
 ctgtgccatc agcctgtggc ttcgagggct gcggatgtgc accccgctgg 250
 ggcgggaagg cgaggagtgc caccgccgca gccacaaggc ccccttcttc 300
 aggaaacgca agcaccacac ctgtccttgc ttgcccaacc tgctgtgctc 350
 caggttcccg gacggcaggt accgctgctc catggacttg aagaacatca 400

atttttaggc gcttgccctgg tctcaggata cccaccatcc ttttcctgag 450
 cacagcctgg atttttattt ctgccatgaa acccagctcc catgactctc 500
 ccagtcacct cactgactac cctgatctct cttgtctagt acgcacatat 550
 gcacacaggg agacatacct cccatcatga catgggtccc aggctggcct 600
 gaggatgtca cagcttgagg ctgtgggtgtg aaagggtggcc agcctgggtc 650
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 tggttaactc cttagtttca gaccacagac tcaagattgg ctcttcccag 950
 agggcagcag acagtacccc caaggcaggt gtagggagcc caggagggcc 1000
 aatcagcccc ctgaagactc tgggtccaggt cagcctgtgg cttgtggcct 1050
 gtgacctgtg accttctgcc agaattgtca tgcctctgag gccccctctt 1100
 accacacttt accagttaac cactgaagcc cccaattccc acagcttttc 1150
 cattaatatg caaatgggtg tggttcaatc taatctgata ttgacatatt 1200
 agaaggcaat taggggtgtt ccttaaacaa ctctttcca aggatcagcc 1250
 ctgagagcag gttgggtgact ttgaggaggg cagtcctctg tccagattgg 1300
 ggtggggagca agggacaggg agcagggcag gggctgaaag gggcactgat 1350
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 caccaactga aaaaa 1415

<210> 371

<211> 105

<212> PRT

<213> Homo sapiens

<400> 371

Met	Arg	Gly	Ala	Thr	Arg	Val	Ser	Ile	Met	Leu	Leu	Leu	Val	Thr
1				5					10					15
Val	Ser	Asp	Cys	Ala	Val	Ile	Thr	Gly	Ala	Cys	Glu	Arg	Asp	Val
				20					25					30
Gln	Cys	Gly	Ala	Gly	Thr	Cys	Cys	Ala	Ile	Ser	Leu	Trp	Leu	Arg
				35					40					45
Gly	Leu	Arg	Met	Cys	Thr	Pro	Leu	Gly	Arg	Glu	Gly	Glu	Glu	Cys
				50					55					60
His	Pro	Gly	Ser	His	Lys	Val	Pro	Phe	Phe	Arg	Lys	Arg	Lys	His
				65					70					75

<210> 373
 <211> 229
 <212> PRT
 <213> Homo sapiens

<400> 373

Met	Ser	Phe	Leu	Gln	Asp	Pro	Ser	Phe	Phe	Thr	Met	Gly	Met	Trp
1				5					10					15
Ser	Ile	Gly	Ala	Gly	Ala	Leu	Gly	Ala	Ala	Ala	Leu	Ala	Leu	Leu
				20					25					30
Leu	Ala	Asn	Thr	Asp	Val	Phe	Leu	Ser	Lys	Pro	Gln	Lys	Ala	Ala
				35					40					45
Leu	Glu	Tyr	Leu	Glu	Asp	Ile	Asp	Leu	Lys	Thr	Leu	Glu	Lys	Glu
				50					55					60
Pro	Arg	Thr	Phe	Lys	Ala	Lys	Glu	Leu	Trp	Glu	Lys	Asn	Gly	Ala
				65					70					75
Val	Ile	Met	Ala	Val	Arg	Arg	Pro	Gly	Cys	Phe	Leu	Cys	Arg	Glu
				80					85					90
Glu	Ala	Ala	Asp	Leu	Ser	Ser	Leu	Lys	Ser	Met	Leu	Asp	Gln	Leu
				95					100					105
Gly	Val	Pro	Leu	Tyr	Ala	Val	Val	Lys	Glu	His	Ile	Arg	Thr	Glu
				110					115					120
Val	Lys	Asp	Phe	Gln	Pro	Tyr	Phe	Lys	Gly	Glu	Ile	Phe	Leu	Asp
				125					130					135
Glu	Lys	Lys	Lys	Phe	Tyr	Gly	Pro	Gln	Arg	Arg	Lys	Met	Met	Phe
				140					145					150
Met	Gly	Phe	Ile	Arg	Leu	Gly	Val	Trp	Tyr	Asn	Phe	Phe	Arg	Ala
				155					160					165
Trp	Asn	Gly	Gly	Phe	Ser	Gly	Asn	Leu	Glu	Gly	Glu	Gly	Phe	Ile
				170					175					180
Leu	Gly	Gly	Val	Phe	Val	Val	Gly	Ser	Gly	Lys	Gln	Gly	Ile	Leu
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Ile	Arg	Thr	Ala	Leu	Gly	Asp	Lys	Ala	Tyr	Ala	Trp	Asp	Thr	Asn	
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Glu	Glu	Tyr	Leu	Phe	Lys	Ala	Met	Val	Ala	Phe	Ser	Met	Arg	Lys	
				50					55					60	
Val	Pro	Asn	Arg	Glu	Ala	Thr	Glu	Ile	Ser	His	Val	Leu	Leu	Cys	
				65					70					75	
Asn	Val	Thr	Gln	Arg	Val	Ser	Phe	Trp	Phe	Val	Val	Thr	Asp	Pro	
				80					85					90	
Ser	Lys	Asn	His	Thr	Leu	Pro	Ala	Val	Glu	Val	Gln	Ser	Ala	Ile	
				95					100					105	
Arg	Met	Asn	Lys	Asn	Arg	Ile	Asn	Asn	Ala	Phe	Phe	Leu	Asn	Asp	
				110					115					120	
Gln	Thr	Leu	Glu	Phe	Leu	Lys	Ile	Pro	Ser	Thr	Leu	Ala	Pro	Pro	
				125					130					135	
Met	Asp	Pro	Ser	Val	Pro	Ile	Trp	Ile	Ile	Ile	Phe	Gly	Val	Ile	
				140					145					150	
Phe	Cys	Ile	Ile	Ile	Val	Ala	Ile	Ala	Leu	Leu	Ile	Leu	Ser	Gly	
				155					160					165	
Ile	Trp	Gln	Arg	Arg	Arg	Lys	Asn	Lys	Glu	Pro	Ser	Glu	Val	Asp	
				170					175					180	
Asp	Ala	Glu	Asp	Lys	Cys	Glu	Asn	Met	Ile	Thr	Ile	Glu	Asn	Gly	
				185					190					195	
Ile	Pro	Ser	Asp	Pro	Leu	Asp	Met	Lys	Gly	Gly	Ile	Leu	Met	Met	
				200					205					210	

Pro Ser

<210> 388

<211> 1371

<212> DNA

<213> Homo sapiens

<400> 388

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gccaaggctg gggttccctc atgtatggca agagctctac tcgtgcggtg 150
cttcttctcc ttggcataca gctcacagct ctttggccta tagcagctgt 200
ggaaatttat acctcccggtg tgctggagga tgtaaatggg acagatgctc 250
ggttaaaatg cactttctcc agctttgccc ctgtgggtga tgctctaaca 300
gtgacctgga attttcgtcc tctagacggg ggacctgagc agtttgtatt 350
ctactaccac atagatccct tccaacccat gagtggcggt ttttaaggacc 400
gggtgtcttg ggatgggaat cctgagcggg acgatgcctc catccttctc 450
tggaactgc agttcgacga caatgggaca tacacctgcc aggtgaagaa 500
cccacctgat gttgatgggg tgatagggga gatccggctc agcgtcgtgc 550
aactgtacg cttctctgag atccacttcc tggctctggc cattggctct 600
gcctgtgcac tgatgatcat aatagtaatt gtagtgggtc tcttcagca 650
ttaccgaaa aagcgatggg ccgaaagagc tcataaagtg gtggagataa 700
aatcaaaaga agaggaaagg ctcaaccaag agaaaaaggc ctctgtttat 750
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aaaggggata aaagccaatt tgtctgttac atttcctttc acgtatttct 1150
tttagcagca cttctgctac taaagttaat gtgtttactc tctttccttc 1200
ccacattctc aattaaaagg tgagctaagc ctctcggtg tttctgatta 1250
acagtaaata ctaaattcaa actgttaaat gacattttta tttttatgtc 1300
tctccttaac tatgagacac atcttgtttt actgaatttc tttcaatatt 1350
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<210> 389

<211> 215

<212> PRT

<213> Homo sapiens

<400> 389

Met	Tyr	Gly	Lys	Ser	Ser	Thr	Arg	Ala	Val	Leu	Leu	Leu	Leu	Gly
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Ile	Gln	Leu	Thr	Ala	Leu	Trp	Pro	Ile	Ala	Ala	Val	Glu	Ile	Tyr	
				20					25					30	
Thr	Ser	Arg	Val	Leu	Glu	Ala	Val	Asn	Gly	Thr	Asp	Ala	Arg	Leu	
				35					40					45	
Lys	Cys	Thr	Phe	Ser	Ser	Phe	Ala	Pro	Val	Gly	Asp	Ala	Leu	Thr	
				50					55					60	
Val	Thr	Trp	Asn	Phe	Arg	Pro	Leu	Asp	Gly	Gly	Pro	Glu	Gln	Phe	
				65					70					75	
Val	Phe	Tyr	Tyr	His	Ile	Asp	Pro	Phe	Gln	Pro	Met	Ser	Gly	Arg	
				80					85					90	
Phe	Lys	Asp	Arg	Val	Ser	Trp	Asp	Gly	Asn	Pro	Glu	Arg	Tyr	Asp	
				95					100					105	
Ala	Ser	Ile	Leu	Leu	Trp	Lys	Leu	Gln	Phe	Asp	Asp	Asn	Gly	Thr	
				110					115					120	
Tyr	Thr	Cys	Gln	Val	Lys	Asn	Pro	Pro	Asp	Val	Asp	Gly	Val	Ile	
				125					130					135	
Gly	Glu	Ile	Arg	Leu	Ser	Val	Val	His	Thr	Val	Arg	Phe	Ser	Glu	
				140					145					150	
Ile	His	Phe	Leu	Ala	Leu	Ala	Ile	Gly	Ser	Ala	Cys	Ala	Leu	Met	
				155					160					165	
Ile	Ile	Ile	Val	Ile	Val	Val	Val	Leu	Phe	Gln	His	Tyr	Arg	Lys	
				170					175					180	
Lys	Arg	Trp	Ala	Glu	Arg	Ala	His	Lys	Val	Val	Glu	Ile	Lys	Ser	
				185					190					195	
Lys	Glu	Glu	Glu	Arg	Leu	Asn	Gln	Glu	Lys	Lys	Val	Ser	Val	Tyr	
				200					205					210	
Leu	Glu	Asp	Thr	Asp											
				215											

<210> 390
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 390
 ccgaggccat ctagaggcca gagc 24

<210> 391
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 391
 acaggcagag ccaatggcca gagc 24

<210> 392
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 392
 gagaggactg cgggagtttg ggacctttgt gcagacgtgc tcatg 45

<210> 393
 <211> 471
 <212> DNA
 <213> Homo sapiens

<400> 393
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 agcagtcctg gtactcttgg gagtttccat ctttctggtc tctgcccaga 100
 atccgacaac agctgctcca gctgacacgt atccagctac tggtcctgct 150
 gatgatgaag cccctgatgc tgaaccact gctgctgcaa ccactgogac 200
 cactgctgct cctaccactg caaccaccgc tgcttctacc actgctcgta 250
 aagacattcc agttttaccc aaatggggtg gggatctccc gaatggtaga 300
 gtgtgtccct gagatggaat cagcttgagt cttctgcaat tggtcacaac 350
 tattcatgct tcctgtgatt tcattccaact acttaccttg cctacgatat 400
 cccctttatc tctaatacgt ttattttctt tcaaataaaa aataactatg 450
 agcaacataa aaaaaaaaaa a 471

<210> 394
 <211> 90
 <212> PRT
 <213> Homo sapiens

<400> 394
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 1 5 10 15
 Leu Val Ser Ala Gln Asn Pro Thr Thr Ala Ala Pro Ala Asp Thr
 20 25 30
 Tyr Pro Ala Thr Gly Pro Ala Asp Asp Glu Ala Pro Asp Ala Glu
 35 40 45
 Thr Thr Ala Ala Ala Thr Thr Ala Thr Thr Ala Ala Pro Thr Thr
 50 55 60
 Ala Thr Thr Ala Ala Ser Thr Thr Ala Arg Lys Asp Ile Pro Val
 65 70 75
 Leu Pro Lys Trp Val Gly Asp Leu Pro Asn Gly Arg Val Cys Pro
 80 85 90

<210> 395
 <211> 25

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 395
gctccctgat cttcatgtca ccacc 25

<210> 396
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 396
cagggacaca ctctaccatt cgggag 26

<210> 397
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 397
ccatctttct ggtctctgcc cagaatccga caacagctgc tc 42

<210> 398
<211> 907
<212> DNA
<213> Homo sapiens

<400> 398
ggactctgaa ggtcccaagc agctgctgag gcccccaagg aagtgggtcc 50
aaccttggac coctaggggt ctggatttgc tggttaacaa gataacctga 100
gggcaggacc ccatagggga atgctacctc ctgcccttcc acctgccctg 150
gtgttcacgg tggcctggtc cctccttgcc gagagagtgt cctgggtcag 200
ggacgcagag gacgctcaca gactccagcc ctttgttacc gagaggacac 250
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gcaggagggg gacagttctg ttgtgcttgg ttggacagta agaggggtctt 350
ggccagtcca ggggtggggg cggcaaactc cataaagaac cagaggggtct 400
gggccccggc cacagagtca tctgccagc tcctctgctg ctggccagtg 450
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gcctgcgggc catgggtccct gtctagggca gcaattctca accttcttgc 550
tctcaggacc ccaaagagct ttcattgtat ctattgattt ttaccacatt 600
agcaattaaa actgagaaat gggccgggca cgggtggctca cgcctgtaat 650

cccagcactt tgggaggccg aggcgggtgg atcacctgag atcaggagtt 700
 caagaccagc ctggccaaca tgggtgaaacc ttgtctacta aaaatacaaa 750
 aaattagcca ggcacagtgg tgtgcaactgg tagtcccagt tactcggggag 800
 gctgaggcag gaaaatcgt tgaacccagg aggcggacgt tgcggtgagc 850
 cgagatcgcg ccgctgattc cagcctgggc gacaagagtg agactccatc 900
 tcacaca 907

<210> 399
 <211> 120
 <212> PRT
 <213> Homo sapiens

<400> 399
 Met Leu Pro Pro Ala Leu Pro Pro Ala Leu Val Phe Thr Val Ala
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 Trp Ser Leu Leu Ala Glu Arg Val Ser Trp Val Arg Asp Ala Glu
 20 25 30
 Asp Ala His Arg Leu Gln Pro Phe Val Thr Glu Arg Thr Leu Gly
 35 40 45
 Lys Val Gln Arg Trp Ser Gly Val His Thr Gln Thr Gly Gly Arg
 50 55 60
 Ala Gly Gly Gly Gln Phe Cys Cys Ala Trp Leu Asp Ser Lys Arg
 65 70 75
 Val Leu Ala Ser Pro Gly Trp Gly Ala Ala Asn Ser Ile Lys Asn
 80 85 90
 Gln Arg Val Trp Ala Pro Ala Thr Glu Ser Ser Ala Gln Leu Leu
 95 100 105
 Cys Cys Trp Pro Val Gly Val Ala Arg Gly Gly Ala Leu Cys Gln
 110 115 120

<210> 400
 <211> 893
 <212> DNA
 <213> Homo sapiens

<400> 400
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 ccggcctgcc tcagcggccc ccatggggcg cccagaactg gcacagcatg 100
 aggagctgac cctgctcttc catgggaccc tgcagctggg ccaggccctc 150
 aacggtgtgt acaggaccac ggagggacgg ctgacaaagg ccaggaacag 200
 cctgggtctc tatggccgca caatagaact cctggggcag gaggtcagcc 250
 ggggccggga tgcagcccag gaacttcggg caagcctgtt ggagactcag 300
 atggaggagg atattctgca gctgcaggca gagggcacag ctgaggtgct 350
 gggggaggtg gcccaggcac agaaggtgct acgggacagc gtgcagcggc 400

tagaagtcca gctgaggagc gcctggctgg gccctgccta ccgagaattt 450
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 cacaggccac gtgcagcggc agaggcggga gatggtggca cagcagcatc 550
 ggctgcgaca gatccaggag agactccaca cagcggcgct cccagcctga 600
 atctgcctgg atggaactga ggaccaatca tgctgcaagg aacacttcca 650
 cgccccgtga ggccccgtg caggaggag ctgcctgttc actgggatca 700
 gccagggcgc cgggccccac ttctgagcac agagcagaga cagacgcagg 750
 cggggacaaa ggcagaggat gtagcccat tggggagggg tggaggaagg 800
 acatgtaccc ttctatgcct acacaccct cattaaagca gagtcgtggc 850
 atttcaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 893

<210> 401
 <211> 198
 <212> PRT
 <213> Homo sapiens

<400> 401
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 Thr Arg Pro Ala Ser Ala Ala Pro Met Gly Gly Pro Glu Leu Ala
 20 25 30
 Gln His Glu Glu Leu Thr Leu Leu Phe His Gly Thr Leu Gln Leu
 35 40 45
 Gly Gln Ala Leu Asn Gly Val Tyr Arg Thr Thr Glu Gly Arg Leu
 50 55 60
 Thr Lys Ala Arg Asn Ser Leu Gly Leu Tyr Gly Arg Thr Ile Glu
 65 70 75
 Leu Leu Gly Gln Glu Val Ser Arg Gly Arg Asp Ala Ala Gln Glu
 80 85 90
 Leu Arg Ala Ser Leu Leu Glu Thr Gln Met Glu Glu Asp Ile Leu
 95 100 105
 Gln Leu Gln Ala Glu Ala Thr Ala Glu Val Leu Gly Glu Val Ala
 110 115 120
 Gln Ala Gln Lys Val Leu Arg Asp Ser Val Gln Arg Leu Glu Val
 125 130 135
 Gln Leu Arg Ser Ala Trp Leu Gly Pro Ala Tyr Arg Glu Phe Glu
 140 145 150
 Val Leu Lys Ala His Ala Asp Lys Gln Ser His Ile Leu Trp Ala
 155 160 165
 Leu Thr Gly His Val Gln Arg Gln Arg Arg Glu Met Val Ala Gln
 170 175 180
 Gln His Arg Leu Arg Gln Ile Gln Glu Arg Leu His Thr Ala Ala

Leu Pro Ala

<210> 402

<211> 1915

<212> DNA

<213> Homo sapiens

<400> 402

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tgtaatttgc atcctggtga tcaccttact cctggaccag accaccagcc 100
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aaggatggag atctgaagac tcaaattgaa aagctctgga cagaagtcaa 200
tgccttgaag gaaattcaag ccctgcagac agtctgtctc cgaggcacta 250
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gaggccaatg aagactgcat ttccaaagga ggaatcctgg ttatccccag 350
gaactccgac gaaatcaacg ccctccaaga ctatggtaaa aggagcctgc 400
caggtgtcaa tgacttttgg ctgggcatca atgacatggc cacggaaggc 450
aagtttggtg acgtcaacgg aatogctatc tccttcctca actgggaccg 500
tgcacagcct aacggtggca agcgagaaaa ctgtgtcctg ttctcccaat 550
cagctcaggg caagtggagt gatgaggcct gtcgcagcag caagagatac 600
atatgcgagt tcaccatccc taaataggtc tttctccaat gtgtcctcca 650
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aatcataatt tttacttatt aaaaaattgc aacacaagat caatgtccat 750
agcaatatga tagcatcagc caattttgct aacacatttc tttgggattt 800
tgcccttcct ggggtatagg ggatcagaaa tattgatcca tgtgcacgca 850
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tgctggcaat aataccttgt cagcccatta cccttatttt gaattgctcc 1150
atctcctggg gggacttgta tottgtctgc catatcagaa cacaaacccc 1200
tgaagagggt ctgatttgat tttttttttt tcttcatgcc tacccttttt 1250
ttggaagttt ccagccgcaa tttgaaatga aatgacaagg tgtatatattg 1300

atcaattttc attcccacca ttgcattaca acctctaact taaatgggta 1350
accctaaggc atatcaaaga agcagattgc atgataaacg gaaatagaaa 1400
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tttttttagc catcattata tgtttaagtc tattatgggc aaccaatctt 1550
tggaagctga aaactgaatt taaagaatgc tatcttggaa aattgcatac 1600
gtctgtgcaa ttttttattc tgcctagtagc tattctgott gtttaactag 1650
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tggagggaaa tgggcttttt agaagcaaac aatttttaa atattttgtt 1750
cttcaaataa atagtgttta aacattgaat gtgttttgtg aacaatatcc 1800
cactttgcaa actttaacta cacatgcttg gaattaagtt ttagctgttt 1850
tcattgctca ataataaagc ctgaattctg atcaataaaa aaaaaaaaaa 1900
aaaaaaaaaa aaaaa 1915

<210> 403

<211> 206

<212> PRT

<213> Homo sapiens

<400> 403

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Val	Ile	Cys	Ile	Leu	Val	Ile	Thr	Leu	Leu	Leu	Asp	Gln	Thr	Thr	20	25	30	
Ser	His	Thr	Ser	Arg	Leu	Lys	Ala	Arg	Lys	His	Ser	Lys	Arg	Arg	35	40	45	
Val	Arg	Asp	Lys	Asp	Gly	Asp	Leu	Lys	Thr	Gln	Ile	Glu	Lys	Leu	50	55	60	
Trp	Thr	Glu	Val	Asn	Ala	Leu	Lys	Glu	Ile	Gln	Ala	Leu	Gln	Thr	65	70	75	
Val	Cys	Leu	Arg	Gly	Thr	Lys	Val	His	Lys	Lys	Cys	Tyr	Leu	Ala	80	85	90	
Ser	Glu	Gly	Leu	Lys	His	Phe	His	Glu	Ala	Asn	Glu	Asp	Cys	Ile	95	100	105	
Ser	Lys	Gly	Gly	Ile	Leu	Val	Ile	Pro	Arg	Asn	Ser	Asp	Glu	Ile	110	115	120	
Asn	Ala	Leu	Gln	Asp	Tyr	Gly	Lys	Arg	Ser	Leu	Pro	Gly	Val	Asn	125	130	135	
Asp	Phe	Trp	Leu	Gly	Ile	Asn	Asp	Met	Val	Thr	Glu	Gly	Lys	Phe	140	145	150	
Val	Asp	Val	Asn	Gly	Ile	Ala	Ile	Ser	Phe	Leu	Asn	Trp	Asp	Arg				

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 ctggagcatc tacacctgag gacaagacgc tgcccacccg cgaggggctga 450
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<210> 408

<211> 104

<212> PRT

<213> Homo sapiens

<400> 408

Met	Lys	Leu	Ala	Ala	Leu	Leu	Gly	Leu	Cys	Val	Ala	Leu	Ser	Cys
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Ser	Ser	Ala	Ala	Ala	Phe	Leu	Val	Gly	Ser	Ala	Lys	Pro	Val	Ala
				20					25					30
Gln	Pro	Val	Ala	Ala	Leu	Glu	Ser	Ala	Ala	Glu	Ala	Gly	Ala	Gly
				35					40					45
Thr	Leu	Ala	Asn	Pro	Leu	Gly	Thr	Leu	Asn	Pro	Leu	Lys	Leu	Leu
				50					55					60
Leu	Ser	Ser	Leu	Gly	Ile	Pro	Val	Asn	His	Leu	Ile	Glu	Gly	Ser
				65					70					75
Gln	Lys	Cys	Val	Ala	Glu	Leu	Gly	Pro	Gln	Ala	Val	Gly	Ala	Val
				80					85					90
Lys	Ala	Leu	Lys	Ala	Leu	Leu	Gly	Ala	Leu	Thr	Val	Phe	Gly	
				95					100					

<210> 409

<211> 2089

<212> DNA

<213> Homo sapiens

<400> 409

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 aaggaggagca ctccttggcc tccgcagccg atcacatgaa ggtggtgcc 100
 agtctcctgc tctccgtcct cctggcacag gtgtggctgg taccggcctt 150
 ggccccagct cctcagtcgc cagagacccc agcccctcag aaccagacca 200
 gcagggtagt gcaggctccc agggaggaag aggaagatga gcaggaggcc 250
 agcgaggaga aggccggtga ggaagagaaa gcctggctga tggccagcag 300
 gcagcagctt gccaaaggaga cttcaaactt cggattcagc ctgctgcaa 350
 agatctccat gaggcacgat ggcaacatgg ttttctctcc atttggcatg 400
 tccttggcca tgacaggctt gatgctgggg gccacagggc cgactgaaac 450
 ccagatcaag agagggtcc acttgaggc cctgaagccc accaagccc 500

His Val Leu Lys	Leu Pro Tyr Gln Gly	Asn Ala Thr Met Leu Val	290	295	300
Val Leu Met Glu	Lys Met Gly Asp His	Leu Ala Leu Glu Asp Tyr	305	310	315
Leu Thr Thr Asp	Leu Val Glu Thr Trp	Leu Arg Asn Met Lys Thr	320	325	330
Arg Asn Met Glu	Val Phe Phe Pro Lys	Phe Lys Leu Asp Gln Lys	335	340	345
Tyr Glu Met His	Glu Leu Leu Arg Gln	Met Gly Ile Arg Arg Ile	350	355	360
Phe Ser Pro Phe	Ala Asp Leu Ser Glu	Leu Ser Ala Thr Gly Arg	365	370	375
Asn Leu Gln Val	Ser Arg Val Leu Arg	Arg Thr Val Ile Glu Val	380	385	390
Asp Glu Arg Gly	Thr Glu Ala Val Ala	Gly Ile Leu Ser Glu Ile	395	400	405
Thr Ala Tyr Ser	Met Pro Pro Val Ile	Lys Val Asp Arg Pro Phe	410	415	420
His Phe Met Ile	Tyr Glu Glu Thr Ser	Gly Met Leu Leu Phe Leu	425	430	435
Gly Arg Val Val	Asn Pro Thr Leu Leu		440		

<210> 411
 <211> 636
 <212> DNA
 <213> Homo sapiens

<400> 411
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 tgtggggaggc aggtgcagtc ccagcaccca aggtccctat caagatgcaa 150
 gtcaaacact ggccctcaga gcaggaccca gagaaggcct ggggcgccc 200
 tgtgggtggag cctccggaga aggacgacca gctgggtggtg ctgttcctg 250
 tccagaagcc gaaactcttg accaccgagg agaagccacg aggtcagggc 300
 agggggcccca tccttccagg caccaaggcc tggatggaga ccgaggacac 350
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 ctccgcctga ggaggaccag ggcgaggaga ggccccggtt gtgggtgatg 450
 ccaaatacc aggtgtcctt gggaccggag gaagaccaag accacatcta 500
 ccacccccag tagggctcca ggggccatca ctgccccgc cctgtcccaa 550
 ggcccaggct gttgggaactg ggaccctccc taccctgccc cagctagaca 600

aataaacccc agcaggcaaa aaaaaaaaaa aaaaaa 636

<210> 412
<211> 151
<212> PRT
<213> Homo sapiens

<400> 412
Met Arg Arg Leu Leu Leu Val Thr Ser Leu Val Val Val Leu Leu
1 5 10 15
Trp Glu Ala Gly Ala Val Pro Ala Pro Lys Val Pro Ile Lys Met
20 25 30
Gln Val Lys His Trp Pro Ser Glu Gln Asp Pro Glu Lys Ala Trp
35 40 45
Gly Ala Arg Val Val Glu Pro Pro Glu Lys Asp Asp Gln Leu Val
50 55 60
Val Leu Phe Pro Val Gln Lys Pro Lys Leu Leu Thr Thr Glu Glu
65 70 75
Lys Pro Arg Gly Gln Gly Arg Gly Pro Ile Leu Pro Gly Thr Lys
80 85 90
Ala Trp Met Glu Thr Glu Asp Thr Leu Gly Arg Val Leu Ser Pro
95 100 105
Glu Pro Asp His Asp Ser Leu Tyr His Pro Pro Pro Glu Glu Asp
110 115 120
Gln Gly Glu Glu Arg Pro Arg Leu Trp Val Met Pro Asn His Gln
125 130 135
Val Leu Leu Gly Pro Glu Glu Asp Gln Asp His Ile Tyr His Pro
140 145 150
Gln

<210> 413
<211> 1176
<212> DNA
<213> Homo sapiens

<400> 413
agaaagctgc actctgttga gctccagggc gcagtggagg gagggagtga 50
aggagctctc tgtacccaag gaaagtgcag ctgagactca gacaagatta 100
caatgaacca actcagcttc ctgctgtttc tcatagcgac caccagagga 150
tggagtacag atgaggctaa tacttacttc aaggaatgga cctgttcttc 200
gtctccatct ctgcccagaa gctgcaagga aatcaaagac gaatgtccta 250
gtgcatttga tggcctgtat tttctccgca ctgagaatgg tgttatctac 300
cagaccttct gtgacatgac ctctgggggt ggcggctgga ccctggtggc 350
cagcgtgcat gagaatgaca tgcgtgggaa gtgcacggtg ggcgatcgct 400

ggtccagtca gcagggcagc aaagcagact acccagaggg ggacggcaac 450
 tgggccaact acaacacctt tggatctgca gaggcggcca cgagcgatga 500
 ctacaagaac cctggctact acgacatcca ggccaaggac ctgggcatct 550
 ggcacgtgcc caataagtcc cccatgcagc actggagaaa cagctccctg 600
 ctgaggtacc gcacggacac tggcttcctc cagacactgg gacataatct 650
 gtttggcatc taccagaaat atccagtga atattggagaa ggaaagtgtt 700
 ggactgacaa cggcccgggtg atccctgtgg tctatgattt tggcgacgcc 750
 cagaaaacag catcttatta ctcaccctat ggccagcggg aattcactgc 800
 gggatttggt cagttcaggg tatttaataa cgagagagca gccaacgcct 850
 tgtgtgctgg aatgaggggtc accggatgta aactgagca tcaactgcatt 900
 ggtggaggag gatactttcc agaggccagt cccagcagt gtggagattt 950
 ttctggtttt gattggagtg gatatggaac tcatgttggt tacagcagca 1000
 gccgtgagat aactgaggca gctgtgcttc tattctatcg ttgagagttt 1050
 tgtgggaggg aaccagacc tctcctccca accatgagat cccaaggatg 1100
 gagaacaact taccagtag ctagaatgtt aatggcagaa gagaaaacaa 1150
 taaatcatat tgactcaaga aaaaaa 1176

<210> 414
 <211> 313
 <212> PRT
 <213> Homo sapiens

<400> 414
 Met Asn Gln Leu Ser Phe Leu Leu Phe Leu Ile Ala Thr Thr Arg
 1 5 10 15
 Gly Trp Ser Thr Asp Glu Ala Asn Thr Tyr Phe Lys Glu Trp Thr
 20 25 30
 Cys Ser Ser Ser Pro Ser Leu Pro Arg Ser Cys Lys Glu Ile Lys
 35 40 45
 Asp Glu Cys Pro Ser Ala Phe Asp Gly Leu Tyr Phe Leu Arg Thr
 50 55 60
 Glu Asn Gly Val Ile Tyr Gln Thr Phe Cys Asp Met Thr Ser Gly
 65 70 75
 Gly Gly Gly Trp Thr Leu Val Ala Ser Val His Glu Asn Asp Met
 80 85 90
 Arg Gly Lys Cys Thr Val Gly Asp Arg Trp Ser Ser Gln Gln Gly
 95 100 105
 Ser Lys Ala Asp Tyr Pro Glu Gly Asp Gly Asn Trp Ala Asn Tyr
 110 115 120
 Asn Thr Phe Gly Ser Ala Glu Ala Ala Thr Ser Asp Asp Tyr Lys

ccacaatagt tcagtgacat ctgctgcttc atcagtaaca atcacaacaa 550
ctatgcattc tgaagcaaag aaaggatcaa aatttgatac tgggagcttt 600
gttggtggtta ttgtattaac gctgggagtt ttatctattc ttacattgg 650
atgcaaaatg tattactcaa gaagaggcat tcggtatcga accatagatg 700
aacatgatgc catcatttaa ggaaatccat ggaccaagga tggaatacag 750
attgatgctg ccctatcaat taattttggt ttattaatag tttaaaacaa 800
tattctcttt ttgaaaatag tataaacagg ccatgcatat aatgtacagt 850
gtattacgta aatatgtaaa gattcttcaa ggtaacaagg gtttggggtt 900
tgaaataaac atctggatct tatagaccgt tcatacaatg gtttttagcaa 950
gttcatagta agacaaacaa gtcctatctt ttttttttgg ctgggggtggg 1000
ggcattggtc acatatgacc agtaattgaa agacgtcatc actgaaagac 1050
agaatgccat ctgggcatac aaataagaag tttgtcacag cactcaggat 1100
tttgggtatc ttttgtagct cacataaaga acttcagtgc ttttcagagc 1150
tgatatatc ttaattacta atgccacaca gaaattatac aatcaaacta 1200
gatctgaagc ataatttaag aaaaacatca acattttttg tgctttaaac 1250
tgtagtagtt ggtctagaaa caaaatactc c 1281

<210> 416

<211> 208

<212> PRT

<213> Homo sapiens

<400> 416

Met	Gly	Leu	Gly	Ala	Arg	Gly	Ala	Trp	Ala	Ala	Leu	Leu	Leu	Gly
1				5				10						15
Thr	Leu	Gln	Val	Leu	Ala	Leu	Leu	Gly	Ala	Ala	His	Glu	Ser	Ala
				20				25						30
Ala	Met	Ala	Ala	Ser	Ala	Asn	Ile	Glu	Asn	Ser	Gly	Leu	Pro	His
				35				40						45
Asn	Ser	Ser	Ala	Asn	Ser	Thr	Glu	Thr	Leu	Gln	His	Val	Pro	Ser
				50				55						60
Asp	His	Thr	Asn	Glu	Thr	Ser	Asn	Ser	Thr	Val	Lys	Pro	Pro	Thr
				65				70						75
Ser	Val	Ala	Ser	Asp	Ser	Ser	Asn	Thr	Thr	Val	Thr	Thr	Met	Lys
				80				85						90
Pro	Thr	Ala	Ala	Ser	Asn	Thr	Thr	Thr	Pro	Gly	Met	Val	Ser	Thr
				95				100						105
Asn	Met	Thr	Ser	Thr	Thr	Leu	Lys	Ser	Thr	Pro	Lys	Thr	Thr	Ser
				110				115						120
Val	Ser	Gln	Asn	Thr	Ser	Gln	Ile	Ser	Thr	Ser	Thr	Met	Thr	Val

	125		130		135
Thr His Asn Ser	Ser Val Thr Ser Ala	Ala Ser Ser Val Thr	Ile		
	140	145	150		
Thr Thr Thr Met	His Ser Glu Ala Lys	Lys Gly Ser Lys Phe	Asp		
	155	160	165		
Thr Gly Ser Phe	Val Gly Gly Ile Val	Leu Thr Leu Gly Val	Leu		
	170	175	180		
Ser Ile Leu Tyr	Ile Gly Cys Lys Met	Tyr Tyr Ser Arg Arg	Gly		
	185	190	195		
Ile Arg Tyr Arg	Thr Ile Asp Glu His	Asp Ala Ile Ile			
	200	205			

<210> 417
 <211> 1728
 <212> DNA
 <213> Homo sapiens

<400> 417
 cagccggggtc ccaagcctgt gcctgagcct gagcctgagc ctgagcccga 50
 gccgggagacc ggtcgcgggg gctccgggct gtgggaccgc tgggccccca 100
 gcgatggcga ccctgtgggg aggccttctt cggcttggct ccttgctcag 150
 cctgtcgtgc ctggcgcttt ccgtgctgct gctggcgag ctgtcagacg 200
 ccgccaagaa tttcgaggat gtcagatgta aatgtatctg ccctccctat 250
 aaagaaaatt ctgggcatat ttataataag aacatatctc agaaagattg 300
 tgattgcctt catgttgtgg agcccatgcc tgtgcggggg cctgatgtag 350
 aagcatactg tctacgctgt gaatgcaa atgaagaaag aagctctgtc 400
 acaatcaagg ttaccattat aatttatctc tccatttttg gccttctact 450
 tctgtacatg gtatatctta ctctggttga gcccatactg aagaggcgcc 500
 tcttttgaca tgcacagttg atacagagt atgatgat tggggatcac 550
 cagccttttg caaatgcaca cgatgtgcta gcccgctccc gcagtcgagc 600
 caacgtgctg aacaaggtag aatatgcaca gcagcgctgg aagcttcaag 650
 tccaagagca gcgaaagtct gtctttgacc ggcatgttgt cctcagctaa 700
 ttgggaattg aattcaaggt gactagaaag aaacaggcag acaactggaa 750
 agaactgact gggttttgct gggtttcatt ttaatacctt gttgatttca 800
 ccaactgttg ctggaagatt caaaactgga agcaaaaact tgcttgattt 850
 ttttttcttg ttaacgtaat aatagagaca tttttaaaag cacacagctc 900
 aaagtcagcc aataagtctt ttcctatttg tgacttttac taataaaaat 950
 aaatctgcct gtaaattatc ttgaagtcct ttacctgga caagcactct 1000

ctttttcacc acatagtttt aacttgactt tcaagataat tttcagggtt 1050
 tttgttggtg ttgttttttg tttgtttggt ttggtgggag aggggagggg 1100
 tgccctgggaa gtgggttaaca acttttttca agtcacttta ctaaacaac 1150
 ttttgtaaag agaccttacc ttctattttc gagtttcatt tatattttgc 1200
 agtgtagcca gcctcatcaa agagctgact tactcatttg acttttgcac 1250
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 atctaaaatg cctgggtggct tttcacaaaa agcagatttt ottcatgtac 1350
 tgtgatgtct gatgcaatgc atcctagaac aaactggcca tttgctagtt 1400
 tactctaaag actaaacata gtcttggtgt gtgtggtctt actcatcttc 1450
 tagtaccttt aaggacaaat cctaaggact tggacacttg caataaagaa 1500
 atttttatatt aaaccaagc ctccctggat tgataatata tacacatttg 1550
 tcagcatttc cggctgtggt gagaggcagc tgtttgagct ccaatatgtg 1600
 cagctttgaa ctagggtctg ggttggtggg gcctcttctg aaagggtctaa 1650
 ccattattgg ataactggct tttttcttcc tatgtcctct ttggaatgta 1700
 acaataaaaa taatttttga aacatcaa 1728

<210> 418
 <211> 198
 <212> PRT
 <213> Homo sapiens

<400> 418
 Met Ala Thr Leu Trp Gly Gly Leu Leu Arg Leu Gly Ser Leu Leu
 1 5 10 15
 Ser Leu Ser Cys Leu Ala Leu Ser Val Leu Leu Leu Ala Gln Leu
 20 25 30
 Ser Asp Ala Ala Lys Asn Phe Glu Asp Val Arg Cys Lys Cys Ile
 35 40 45
 Cys Pro Pro Tyr Lys Glu Asn Ser Gly His Ile Tyr Asn Lys Asn
 50 55 60
 Ile Ser Gln Lys Asp Cys Asp Cys Leu His Val Val Glu Pro Met
 65 70 75
 Pro Val Arg Gly Pro Asp Val Glu Ala Tyr Cys Leu Arg Cys Glu
 80 85 90
 Cys Lys Tyr Glu Glu Arg Ser Ser Val Thr Ile Lys Val Thr Ile
 95 100 105
 Ile Ile Tyr Leu Ser Ile Leu Gly Leu Leu Leu Leu Tyr Met Val
 110 115 120
 Tyr Leu Thr Leu Val Glu Pro Ile Leu Lys Arg Arg Leu Phe Gly
 125 130 135

Arg Phe Pro Pro Met Met His His His Gln Ala Pro Ser Asp Gly
50 55 60

Gln Thr Pro Gly Ala Arg Phe Gln Arg Ser His Leu Ala Glu Ala
65 70 75

Phe Ala Lys Ala Lys Gly Ser Gly Gly Gly Ala Gly Gly Gly Gly
80 85 90

Ser Gly Arg Gly Leu Met Gly Gln Ile Ile Pro Ile Tyr Gly Phe
95 100 105

Gly Ile Phe Leu Tyr Ile Leu Tyr Ile Leu Phe Lys Val Ser Arg
110 115 120

Ile Ile Leu Ile Ile Leu His Gln
125

<210> 421
<211> 1630
<212> DNA
<213> Homo sapiens

<400> 421
cggctcgagt gcagctgtgg ggagatttca gtgcattgcc tcccctgggt 50
gctcttcattc ttggatttga aagttgagag cagcatgttt tgcccactga 100
aactcattcct gctgccagtg ttactggatt attccttggg cctgaatgac 150
ttgaatgttt ccccgccctga gctaacagtc catgtgggtg attcagctct 200
gatgggatgt gttttccaga gcacagaaga caaatgtata ttcaagatag 250
actggactct gtcaccagga gagcacgcca aggacgaata tgtgctatac 300
tattactoca atctcagtgt gcctattggg cgcttccaga accgcgtaca 350
cttgatgggg gacatcttat gcaatgatgg ctctctcctg ctccaagatg 400
tgcaagaggg tgaccaggga acctatatct gtgaaatccg cctcaaaggg 450
gagagccagg tgttcaagaa ggcggtggta ctgcatgtgc ttccagagga 500
gccccaaagag ctcatgggtcc atgtgggtgg attgattcag atgggatgtg 550
ttttccagag cacagaagtg aaacacgtga ccaaggtaga atggatattt 600
tcaggacggc gcgcaaagga ggagattgta tttcgttact accacaaact 650
caggatgtct gtggagtact ccagagctg gggccacttc cagaatcgtg 700
tgaacctggg gggggacatt ttccgcaatg acggttccat catgcttcaa 750
ggagtgaggg agtcagatgg aggaaactac acctgcagta tccacctagg 800
gaacctgggtg ttcaagaaaa ccattgtgct gcatgtcagc ccggaagagc 850
ctcgaacact ggtgaccccg gcagccctga ggcctctggg cttgggtggg 900
aatcagttgg tgatcattgt gggaattgtc tgtgccacaa tcctgctgct 950
ccctgttctg atattgatcg tgaagaagac ctgtggaaat aagagttcag 1000

tgaattctac agtcttggtg aagaacacga agaagactaa tccagagata 1050
 aaagaaaaac cctgccattt tgaaagatgt gaaggggaga aacacattta 1100
 ctccccaata attgtacggg aggtgatcga ggaagaagaa ccaagtgaaa 1150
 aatcagagggc cacctacatg accatgcacc cagtttggcc ttctctgagg 1200
 tcagatcgga acaactcact tgaaaaaaag tcaggtgggg gaatgccaaa 1250
 aacacagcaa gccttttgag aagaatggag agtcccttca tctcagcagc 1300
 ggtggagact ctctcctgtg tgtgtcctgg gccactctac cagtgatttc 1350
 agactcccg c tctccagct gtcctcctgt ctcatgttt ggtcaatata 1400
 ctgaagatgg agaatttggg gcctggcaga gagactggac agctctggag 1450
 gaacaggcct gctgagggga ggggagcatg gacttggcct ctggagtggg 1500
 aactggccc tgggaaccag gctgagctga gtggcctcaa accccccgtt 1550
 ggatcagacc ctctgtggg cagggttctt agtggatgag ttactgggaa 1600
 gaatcagaga taaaaaccaa cccaaatcaa 1630

<210> 422
 <211> 394
 <212> PRT
 <213> Homo sapiens

<400> 422
 Met Phe Cys Pro Leu Lys Leu Ile Leu Leu Pro Val Leu Leu Asp
 1 5 10 15
 Tyr Ser Leu Gly Leu Asn Asp Leu Asn Val Ser Pro Pro Glu Leu
 20 25 30
 Thr Val His Val Gly Asp Ser Ala Leu Met Gly Cys Val Phe Gln
 35 40 45
 Ser Thr Glu Asp Lys Cys Ile Phe Lys Ile Asp Trp Thr Leu Ser
 50 55 60
 Pro Gly Glu His Ala Lys Asp Glu Tyr Val Leu Tyr Tyr Tyr Ser
 65 70 75
 Asn Leu Ser Val Pro Ile Gly Arg Phe Gln Asn Arg Val His Leu
 80 85 90
 Met Gly Asp Ile Leu Cys Asn Asp Gly Ser Leu Leu Leu Gln Asp
 95 100 105
 Val Gln Glu Ala Asp Gln Gly Thr Tyr Ile Cys Glu Ile Arg Leu
 110 115 120
 Lys Gly Glu Ser Gln Val Phe Lys Lys Ala Val Val Leu His Val
 125 130 135
 Leu Pro Glu Glu Pro Lys Glu Leu Met Val His Val Gly Gly Leu
 140 145 150
 Ile Gln Met Gly Cys Val Phe Gln Ser Thr Glu Val Lys His Val

	155		160		165
Thr Lys Val Glu	Trp Ile Phe Ser Gly	Arg Arg Ala Lys Glu	Glu		
	170	175	180		
Ile Val Phe Arg	Tyr Tyr His Lys Leu	Arg Met Ser Val Glu	Tyr		
	185	190	195		
Ser Gln Ser Trp	Gly His Phe Gln Asn	Arg Val Asn Leu Val	Gly		
	200	205	210		
Asp Ile Phe Arg	Asn Asp Gly Ser Ile	Met Leu Gln Gly Val	Arg		
	215	220	225		
Glu Ser Asp Gly	Gly Asn Tyr Thr Cys	Ser Ile His Leu Gly	Asn		
	230	235	240		
Leu Val Phe Lys	Lys Thr Ile Val Leu	His Val Ser Pro Glu	Glu		
	245	250	255		
Pro Arg Thr Leu	Val Thr Pro Ala Ala	Leu Arg Pro Leu Val	Leu		
	260	265	270		
Gly Gly Asn Gln	Leu Val Ile Ile Val	Gly Ile Val Cys Ala	Thr		
	275	280	285		
Ile Leu Leu Leu	Pro Val Leu Ile Leu	Ile Val Lys Lys Thr	Cys		
	290	295	300		
Gly Asn Lys Ser	Ser Val Asn Ser Thr	Val Leu Val Lys Asn	Thr		
	305	310	315		
Lys Lys Thr Asn	Pro Glu Ile Lys Glu	Lys Pro Cys His Phe	Glu		
	320	325	330		
Arg Cys Glu Gly	Glu Lys His Ile Tyr	Ser Pro Ile Ile Val	Arg		
	335	340	345		
Glu Val Ile Glu	Glu Glu Glu Pro Ser	Glu Lys Ser Glu Ala	Thr		
	350	355	360		
Tyr Met Thr Met	His Pro Val Trp Pro	Ser Leu Arg Ser Asp	Arg		
	365	370	375		
Asn Asn Ser Leu	Glu Lys Lys Ser Gly	Gly Gly Met Pro Lys	Thr		
	380	385	390		
Gln Gln Ala Phe					

<210> 423

<211> 963

<212> DNA

<213> Homo sapiens

<400> 423

ctatgaagaa gcttcctgga aaacaataag caaaggaaaa caaatgtgtc 50

ccatctcaca tggttctacc ctactaaaga caggaagatc ataaactgac 100

agataactgaa attgtaagag ttggaaaacta cattttgcaa agtcattgaa 150

ctctgagctc agttgcagta ctcggaagc catgcaggat gaagatggat 200

acatcacctt aaatattaaa actcggaac cagctctcgt ctccgttggc 250
 cctgcatcct cctcctggtg gcgtgtgatg gctttgattc tgctgatcct 300
 gtgcgtgggg atggttgtcg ggctggtggc tctggggatt tggctctgtca 350
 tgcagcgcaa ttacctacaa gatgagaatg aaaatcgcac aggaactctg 400
 caacaattag caaagcgctt ctgtcaatat gtggtaaaac aatcagaact 450
 aaagggaact ttcaaaggtc ataaatgcag cccctgtgac acaaactgga 500
 gatattatgg agatagctgc tatgggttct tcaggcacia cttaacatgg 550
 gaagagagta agcagtactg cactgacatg aatgctactc tcctgaagat 600
 tgacaaccgg aacattgtgg agtacatcaa agccaggact catttaattc 650
 gttgggtcgg attatctcgc cagaagtcga atgaggtctg gaagtgggag 700
 gatggctcgg ttatctcaga aaatatgttt gagtttttgg aagatggaaa 750
 aggaaatatg aattgtgott attttcataa tgggaaaatg caccctacct 800
 tctgtgagaa caaacattat ttaatgtgtg agaggaaggc tggcatgacc 850
 aagggtggacc aactacctta atgcaaagag gtggacagga taacacagat 900
 aagggtttta ttgtacaata aaagatatgt atgaatgcat cagtagctga 950
 aaaaaaaaaaaa aaa 963

<210> 424
 <211> 229
 <212> PRT
 <213> Homo sapiens

<400> 424
 Met Gln Asp Glu Asp Gly Tyr Ile Thr Leu Asn Ile Lys Thr Arg
 1 5 10 15
 Lys Pro Ala Leu Val Ser Val Gly Pro Ala Ser Ser Ser Trp Trp
 20 25 30
 Arg Val Met Ala Leu Ile Leu Leu Ile Leu Cys Val Gly Met Val
 35 40 45
 Val Gly Leu Val Ala Leu Gly Ile Trp Ser Val Met Gln Arg Asn
 50 55 60
 Tyr Leu Gln Asp Glu Asn Glu Asn Arg Thr Gly Thr Leu Gln Gln
 65 70 75
 Leu Ala Lys Arg Phe Cys Gln Tyr Val Val Lys Gln Ser Glu Leu
 80 85 90
 Lys Gly Thr Phe Lys Gly His Lys Cys Ser Pro Cys Asp Thr Asn
 95 100 105
 Trp Arg Tyr Tyr Gly Asp Ser Cys Tyr Gly Phe Phe Arg His Asn
 110 115 120
 Leu Thr Trp Glu Glu Ser Lys Gln Tyr Cys Thr Asp Met Asn Ala

<400> 428
 ccaccaatgg cagccccacc t 21

 <210> 429
 <211> 17
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 429
 gactgccctc cctgcca 17

 <210> 430
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 430
 caaaaagcct ggaagtcttc aaag 24

 <210> 431
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 431
 cagctggact gcaggtgcta 20

 <210> 432
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 432
 cagtgagcac agcaagtgtc ct 22

 <210> 433
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 433
 ggccacctcc ttgagtcttc agttccct 28

 <210> 434
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

 <400> 434
 caactactgg ctaaagctgg tgaa 24

 <210> 435
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 435
 cctttctgta taggtgatac ccaatga 27

 <210> 436
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 436
 tggccatccc taccagaggc aaaa 24

 <210> 437
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 437
 ctgaagacga cgcggattac ta 22

 <210> 438
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 438
 ggcagaaatg ggaggcaga 19

 <210> 439
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 439
 tgctctgttg gctacggctt tagtccctag 30

 <210> 440
 <211> 22

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 440
 agcagcagcc atgtagaatg aa 22

 <210> 441
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 441
 aatacgaaca gtgcacgctg at 22

 <210> 442
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 442
 tccagagagc caagcacggc aga 23

 <210> 443
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 443
 tctagccagc ttggctccaa ta 22

 <210> 444
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 444
 cctggctcta gcaccaactc ata 23

 <210> 445
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 445
 tcagtggccc taaggagatg ggcct 25

<210> 446
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 446
 caggatacag tgggaatctt gaga 24

 <210> 447
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 447
 cctgaagggc ttggagctta gt 22

 <210> 448
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 448
 tctttggcca tttcccatgg ctca 24

 <210> 449
 <211> 18
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 449
 cccatggcga ggaggaat 18

 <210> 450
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 450
 tgcgtacgtg tgccttcag 19

 <210> 451
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

<400> 451
cagcacccca ggcagtctgt gtgt 24

<210> 452
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 452
aacgtgctac acgaccagtg tact 24

<210> 453
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 453
cacagcatat tcagatgact aaatcca 27

<210> 454
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 454
ttgttttagtt ctccaccgtg tctccacaga a 31

<210> 455
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 455
tgtcagaatg caacctggct t 21

<210> 456
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 456
tgatgtgcct ggctcagaac 20

<210> 457
<211> 24
<212> DNA
<213> Artificial Sequence

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<220>
<223> Synthetic oligonucleotide probe

<400> 457
    tgcacctaga tgtccccagc accc 24

<210> 458
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 458
    aagatgcgcc aggcttctta 20

<210> 459
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 459
    ctctgtacg gtctgctcac ttat 24

<210> 460
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 460
    tggctgtcag tccagtgtgc atgg 24

<210> 461
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 461
    gcatagggat agataagatc ctgctttat 29

<210> 462
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 462
    caaattaàag tacccatcag gagagaa 27

<210> 463
<211> 37

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<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 463
 aagttgctaa atatatacat tatctgcgcc aagtcca 37

 <210> 464
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 464
 gtgctgccca caattcatga 20

 <210> 465
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 465
 gtccttggtgta tgggtctgaa ttatat 26

 <210> 466
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 466
 actctctgca cccacagtc accactatct c 31

 <210> 467
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 467
 ctgaggaacc agccatgtct ct 22

 <210> 468
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 <212> DNA
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 <220>
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 <400> 468
 gaccagatgc aggtacagga tga 23

<210> 469
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 <212> DNA
 <213> Artificial Sequence

 <220>
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 <400> 469
 ctgccccttc agtgatgcca acctt 25

 <210> 470
 <211> 22
 <212> DNA
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 <220>
 <223> Synthetic oligonucleotide probe

 <400> 470
 ggggtggaggc tcactgagta ga 22

 <210> 471
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 471
 caatacagggt aatgaaactc tgcttctt 28

 <210> 472
 <211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 472
 tcctctttaag cataggccat tttctcagtt tagaca 36

 <210> 473
 <211> 21
 <212> DNA
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 <220>
 <223> Synthetic oligonucleotide probe

 <400> 473
 ggtggtcttg cttggtctca c 21

 <210> 474
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

<400> 474
 ccgtcgttca gcaacatgac 20

 <210> 475
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 475
 accgcctacc gctgtgccca 20

 <210> 476
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 <212> DNA
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 <220>
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 <400> 476
 cagtaaaacc acaggctgga ttt 23

 <210> 477
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 <220>
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 <400> 477
 cctgagagca agaaggttga gaat 24

 <210> 478
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 478
 tagacaggga ccatggcccg ca 22

 <210> 479
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 479
 tgggctgtag aagagttggt g 21

 <210> 480
 <211> 20
 <212> DNA
 <213> Artificial Sequence

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<220>
<223> Synthetic oligonucleotide probe

<400> 480
    tccacacttg gccagtttat 20

<210> 481
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 481
    cccaacttct cccttttgga ccct 24

<210> 482
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 482
    gtcccttcac tgttttagagc atga 24

<210> 483
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 483
    actctccccc tcaacagcct cctgag 26

<210> 484
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 484
    gtggtcaggg cagatccttt 20

<210> 485
<211> 23
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<220>
<223> Synthetic oligonucleotide probe

<400> 485
    acagatccag gagagactcc aca 23

<210> 486
<211> 21

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<212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 486
 agcggcgctc ccagcctgaa t 21

 <210> 487
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 487
 catgattggc cctcagttcc atc 23

 <210> 488
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 488
 atagagggct cccagaagtg 20

 <210> 489
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 489
 cagggccttc agggccttca c 21

 <210> 490
 <211> 19
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 490
 gctcagccaa acactgtca 19

 <210> 491
 <211> 17
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic oligonucleotide probe

 <400> 491
 ggggccctga cagtgtt 17

<210> 492
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 492
ctgagccgag actggagcat ctacac 26

<210> 493
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 493
gtgggcagcg tcttgtc 17

<210> 494
<211> 1231
<212> DNA
<213> Homo Sapien

<400> 494
cccacgcgtc cgcgcagtcg cgcagttctg cctccgcctg ccagtctcgc 50
ccgcgatccc ggcccggggc tgtggcgctg actccgaccc aggcagccag 100
cagcccgcgc gggagccgga ccgccgccgg aggagctcgg acggcatgct 150
gagccccctc ctttgctgaa gcccgagtgc ggagaagccc gggcaaacgc 200
aggctaagga gaccaaagcg gcgaagtgc gagacagcgg acaagcagcg 250
gaggagaagg aggaggaggc gaaccagag aggggcagca aaagaagcgg 300
tggtggtggg cgtcgtggcc atggggcgcg ctatcgccag ctcgctcatc 350
cgtcagaaga ggcaagcccg cgagcgcgag aaatccaacg cctgcaagtg 400
tgtcagcagc ccagcaaag gcaagaccag ctgcgacaaa aacaagttaa 450
atgtcttttc ccgggtcaaa ctcttcggct ccaagaagag gcgcagaaga 500
agaccagagc ctcagcttaa gggatatgtt accaagctat acagccgaca 550
aggctaccac ttgcagctgc aggcggatgg aaccattgat ggcaccaaag 600
atgaggacag cacttacact ctgtttaacc tcatccctgt gggctctgcga 650
gtggtggcta tccaaggagt tcaaaccaag ctgtacttgg caatgaacag 700
tgagggatac ttgtacacct cggaactttt cacacctgag tgcaaattca 750
aagaatcagt gtttgaaaat tattatgtga catattcatc aatgatatac 800
cgtcagcagc agtcaggccg aggggtggtat ctgggtctga acaaagaagg 850
agagatcatg aaaggcaacc atgtgaagaa gaacaagcct gcagctcatt 900

ttctgcctaa accactgaaa gtggccatgt acaaggagcc atcactgcac 950
gatctcacgg agttctcccg atctggaagc gggaccccaa ccaagagcag 1000
aagtgtctct ggcggtgctga acggaggcaa atccatgagc cacaatgaat 1050
caacgtagcc agtgagggca aaagaagggc tctgtaacag aaccttacct 1100
ccagggtgctg ttgaattctt ctagcagtc ttcacccaaa agttcaaatt 1150
tgtcagtgac atttaccaaaa caaacaggca gagttcacta ttctatctgc 1200
cattagacct tcttatcatc cataactaaag c 1231

<210> 495
<211> 245
<212> PRT
<213> Homo Sapien

<400> 495
Met Ala Ala Ala Ile Ala Ser Ser Leu Ile Arg Gln Lys Arg Gln
1 5 10 15
Ala Arg Glu Arg Glu Lys Ser Asn Ala Cys Lys Cys Val Ser Ser
20 25 30
Pro Ser Lys Gly Lys Thr Ser Cys Asp Lys Asn Lys Leu Asn Val
35 40 45
Phe Ser Arg Val Lys Leu Phe Gly Ser Lys Lys Arg Arg Arg Arg
50 55 60
Arg Pro Glu Pro Gln Leu Lys Gly Ile Val Thr Lys Leu Tyr Ser
65 70 75
Arg Gln Gly Tyr His Leu Gln Leu Gln Ala Asp Gly Thr Ile Asp
80 85 90
Gly Thr Lys Asp Glu Asp Ser Thr Tyr Thr Leu Phe Asn Leu Ile
95 100 105
Pro Val Gly Leu Arg Val Val Ala Ile Gln Gly Val Gln Thr Lys
110 115 120
Leu Tyr Leu Ala Met Asn Ser Glu Gly Tyr Leu Tyr Thr Ser Glu
125 130 135
Leu Phe Thr Pro Glu Cys Lys Phe Lys Glu Ser Val Phe Glu Asn
140 145 150
Tyr Tyr Val Thr Tyr Ser Ser Met Ile Tyr Arg Gln Gln Gln Ser
155 160 165
Gly Arg Gly Trp Tyr Leu Gly Leu Asn Lys Glu Gly Glu Ile Met
170 175 180
Lys Gly Asn His Val Lys Lys Asn Lys Pro Ala Ala His Phe Leu
185 190 195
Pro Lys Pro Leu Lys Val Ala Met Tyr Lys Glu Pro Ser Leu His
200 205 210
Asp Leu Thr Glu Phe Ser Arg Ser Gly Ser Gly Thr Pro Thr Lys

	215		220		225
Ser Arg Ser Val Ser Gly Val Leu Asn Gly Gly Lys Ser Met Ser					
	230		235		240
His Asn Glu Ser Thr					
	245				

<210> 496
 <211> 1471
 <212> DNA
 <213> Homo Sapien

<400> 496
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 gacatggggg ggacttggtg aaaaaggtat tatccagcca gagggctctgg 100
 gagccctgtc ttactgaacc tgggcaacct ggatattctg agacataattt 150
 tggggggatt tcagtgaaaa aagtggggga tcccctccat ttagagtgtg 200
 gcaaaggaaa aaacaccaag gttgggttcc ttcctgacat tggcagtgcc 250
 ccagtagggg tgggatgagc gaatattccc aaagctaaag tcccacaccc 300
 tgtagattac aagagtggat ttggcaggag tgtgccccaa aatacagtgg 350
 aaaggtgcct gaagataattt aaaccacgtc ttggaaattt agtgggtctt 400
 ggctttggga taggtgaagt gaggacagac actggagagg agggaaaggg 450
 gacgttttca ataggaggca aaactcgagg gtgggatcca ctgaggagta 500
 cataggctgc tggatctggt ggagccagca ctgggcccac gggtggtaac 550
 tggctgctgt ggaggggggt acgtgagggg ggggtctggg gcttatcctc 600
 aggtcctgtg ggtggggcag cgagtcgggg cctgagcgtc aagagcatgc 650
 cctagtgagc gggctcctct gggggagccc agcgcgctcc gggcgctgc 700
 cggtttgggg gtgtctcctc ccggggcgct atggcgggcg tggccagtag 750
 cctgatccgg cagaagcggg aggtccgcga gcccgggggc agccggccgg 800
 tgtcggcgca gcggcgctg tgtcccgcg gcaccaagtc cctttgccag 850
 aagcagctcc tcatcctgct gtccaagggt cgactgtgcg gggggcggcc 900
 cgcgcgggcg gacgcgggcc cggagcctca gctcaaaggc atcgtcacca 950
 aactgttctg ccgccagggt ttctacctcc aggcgaatcc cgacggaagc 1000
 atccagggca cccagagga taccagctcc ttcacccact tcaacctgat 1050
 ccctgtgggc ctccgtgtgg tcaccatcca gagcgccaag ctgggtcact 1100
 acatggccat gaatgctgag ggactgctct acagttcgcc gcatttcaca 1150
 gctgagtgtc gctttaagga gtgtgtcttt gagaattact acgtcctgta 1200
 cgcctctgct ctctaccgcc agcgtcgttc tggccggggc tggtagctcg 1250

gcctggacaa ggagggccag gtcataagg gaaaccgagt taagaagacc 1300
aaggcagctg cccactttct gcccaagctc ctggaggtgg ccatgtacca 1350
ggagccttct ctccacagtg tccccgaggc ctcccccttc agtccccctg 1400
ccccctgaaa tgtagtccct ggactggagg ttccctgcac tcccagtgag 1450
ccagccacca ccacaacctg t 1471

<210> 497
<211> 225
<212> PRT
<213> Homo Sapien

<400> 497
Met Ala Ala Leu Ala Ser Ser Leu Ile Arg Gln Lys Arg Glu Val
1 5 10 15
Arg Glu Pro Gly Gly Ser Arg Pro Val Ser Ala Gln Arg Arg Val
20 25 30
Cys Pro Arg Gly Thr Lys Ser Leu Cys Gln Lys Gln Leu Leu Ile
35 40 45
Leu Leu Ser Lys Val Arg Leu Cys Gly Gly Arg Pro Ala Arg Pro
50 55 60
Asp Arg Gly Pro Glu Pro Gln Leu Lys Gly Ile Val Thr Lys Leu
65 70 75
Phe Cys Arg Gln Gly Phe Tyr Leu Gln Ala Asn Pro Asp Gly Ser
80 85 90
Ile Gln Gly Thr Pro Glu Asp Thr Ser Ser Phe Thr His Phe Asn
95 100 105
Leu Ile Pro Val Gly Leu Arg Val Val Thr Ile Gln Ser Ala Lys
110 115 120
Leu Gly His Tyr Met Ala Met Asn Ala Glu Gly Leu Leu Tyr Ser
125 130 135
Ser Pro His Phe Thr Ala Glu Cys Arg Phe Lys Glu Cys Val Phe
140 145 150
Glu Asn Tyr Tyr Val Leu Tyr Ala Ser Ala Leu Tyr Arg Gln Arg
155 160 165
Arg Ser Gly Arg Ala Trp Tyr Leu Gly Leu Asp Lys Glu Gly Gln
170 175 180
Val Met Lys Gly Asn Arg Val Lys Lys Thr Lys Ala Ala Ala His
185 190 195
Phe Leu Pro Lys Leu Leu Glu Val Ala Met Tyr Gln Glu Pro Ser
200 205 210
Leu His Ser Val Pro Glu Ala Ser Pro Ser Ser Pro Pro Ala Pro
215 220 225

<210> 498
<211> 744

<212> DNA
<213> Homo Sapien

<400> 498

atggccgcgg ccacgcctag cggcttgatc cgccagaagc ggcaggcgcg 50
ggagcagcac tgggaccggc cgtctgccag caggaggcgg agcagcccca 100
gcaagaaccg cgggctctgc aacggcaacc tgggtggatat cttctccaaa 150
gtgcgcacatc tgggcctcaa gaagcgcagg ttgcggcgcc aagatcccca 200
gctcaagggg atagtgaaca ggttatattg caggcaaggc tactacttgc 250
aaatgcaccc cgatggagct ctcatggaa ccaaggatga cagcactaat 300
tctacactct tcaacctcat accagtggga ctacgtgttg ttgccatcca 350
gggagtgaac acaggggtgt atatagccat gaatggagaa gggtacctct 400
acccatcaga actttttacc cctgaatgca agtttaaaga atctgttttt 450
gaaaattatt atgtaatcta ctcatccatg ttgtacagac aacaggaatc 500
tggtagagcc tgggttttgg gattaaataa ggaagggcaa gctatgaaag 550
ggaacagagt aaagaaaacc aaaccagcag ctcattttct acccaagcca 600
ttggaagtgt ccatgtaccg agaaccatct ttgcatgatg ttggggaaac 650
gggtcccgaag cctgggggtga cgccaagtaa aagcacaagt gcgtctgcaa 700
taatgaatgg aggcaaacca gtcaacaaga gtaagacaac atag 744

<210> 499

<211> 247

<212> PRT

<213> Homo Sapien

<400> 499

Met	Ala	Ala	Ala	Ile	Ala	Ser	Gly	Leu	Ile	Arg	Gln	Lys	Arg	Gln	1	5	10	15
Ala	Arg	Glu	Gln	His	Trp	Asp	Arg	Pro	Ser	Ala	Ser	Arg	Arg	Arg	20	25	30	
Ser	Ser	Pro	Ser	Lys	Asn	Arg	Gly	Leu	Cys	Asn	Gly	Asn	Leu	Val	35	40	45	
Asp	Ile	Phe	Ser	Lys	Val	Arg	Ile	Phe	Gly	Leu	Lys	Lys	Arg	Arg	50	55	60	
Leu	Arg	Arg	Gln	Asp	Pro	Gln	Leu	Lys	Gly	Ile	Val	Thr	Arg	Leu	65	70	75	
Tyr	Cys	Arg	Gln	Gly	Tyr	Tyr	Leu	Gln	Met	His	Pro	Asp	Gly	Ala	80	85	90	
Leu	Asp	Gly	Thr	Lys	Asp	Asp	Ser	Thr	Asn	Ser	Thr	Leu	Phe	Asn	95	100	105	
Leu	Ile	Pro	Val	Gly	Leu	Arg	Val	Val	Ala	Ile	Gln	Gly	Val	Lys	110	115	120	

Thr	Gly	Leu	Tyr	Ile	Ala	Met	Asn	Gly	Glu	Gly	Tyr	Leu	Tyr	Pro
				125					130					135
Ser	Glu	Leu	Phe	Thr	Pro	Glu	Cys	Lys	Phe	Lys	Glu	Ser	Val	Phe
				140					145					150
Glu	Asn	Tyr	Tyr	Val	Ile	Tyr	Ser	Ser	Met	Leu	Tyr	Arg	Gln	Gln
				155					160					165
Glu	Ser	Gly	Arg	Ala	Trp	Phe	Leu	Gly	Leu	Asn	Lys	Glu	Gly	Gln
				170					175					180
Ala	Met	Lys	Gly	Asn	Arg	Val	Lys	Lys	Thr	Lys	Pro	Ala	Ala	His
				185					190					195
Phe	Leu	Pro	Lys	Pro	Leu	Glu	Val	Ala	Met	Tyr	Arg	Glu	Pro	Ser
				200					205					210
Leu	His	Asp	Val	Gly	Glu	Thr	Val	Pro	Lys	Pro	Gly	Val	Thr	Pro
				215					220					225
Ser	Lys	Ser	Thr	Ser	Ala	Ser	Ala	Ile	Met	Asn	Gly	Gly	Lys	Pro
				230					235					240
Val	Asn	Lys	Ser	Lys	Thr	Thr								
				245										

<210> 500
 <211> 2906
 <212> DNA
 <213> Homo Sapien

<400> 500
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 ggctgttggg tgccttgcaa aaatgaagga tgcaggacgc agctttctcc 100
 tggaaccgaa cgcaatggat aaactgattg tgcaagagag aaggaagaac 150
 gaagcttttt cttgtgagcc ctggatctta acacaaatgt gtatatgtgc 200
 acacagggag cattcaagaa tgaaataaac cagagttaga cccgcggggg 250
 ttggtgtgtt ctgacataaa taaataatct taaagcagct gttcccctcc 300
 ccacccccaa aaaaaaggat gattggaaat gaagaaccga ggattcaca 350
 agaaaaaagt atgttcattt ttctctataa aggagaaagt gagccaagga 400
 gatatttttg gaatgaaaag tttggggcct ttttagtaaa gtaaagaact 450
 ggtgtggtgg tgttttcctt tctttttgaa tttcccacaa gaggagagga 500
 aattaataat acatctgcaa agaaatttca gagaagaaaa gttgaccgcg 550
 gcagattgag gcattgattg ggggagagaa accagcagag cacagttgga 600
 tttgtgccta tgttgactaa aattgacgga taattgcagt tggatttttc 650
 ttcattcaacc tccttttttt taaattttta ttccttttgg tatcaagatc 700
 atgcgttttc tcttgttctt aaccacctgg atttccatct ggatgttgct 750

agtgggatcc caggaattga tgaggtcatg aagactacca aaatcatcat 2400
 tgggtgtttt gtggccatca cactcatggc tgcagtgatg ctggtcattt 2450
 tctacaagat gaggaagcag caccatcggc aaaaccatca cgccccaaca 2500
 aggactgttg aaattattaa tgtggatgat gagattacgg gagacacacc 2550
 catggaaagc cacctgcccc tgcctgctat cgagcatgag cacctaaatc 2600
 actataactc atacaaatct cccttcaacc acacaacaac agttaacaca 2650
 ataaattcaa tacacagttc agtgcatgaa ccgttattga tccgaatgaa 2700
 ctctaaagac aatgtacaag agactcaaat ctaaaacatt tacagagtta 2750
 caaaaaacaa acaatcaaaa aaaaagacag tttattaaaa atgacacaaa 2800
 tgactggggt aaatctactg tttcaaaaaa gtgtctttac aaaaaaacia 2850
 aaaagaaaag aaatttattt attaaaaatt ctattgtgat ctaaagcaga 2900
 caaaaa 2906

<210> 501
 <211> 640
 <212> PRT
 <213> Homo Sapien

<400> 501
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 Pro Arg Phe Asn Arg Ala Leu Phe Asp Pro Leu Leu Val Val Leu
 20 25 30
 Leu Ala Leu Gln Leu Leu Val Val Ala Gly Leu Val Arg Ala Gln
 35 40 45
 Thr Cys Pro Ser Val Cys Ser Cys Ser Asn Gln Phe Ser Lys Val
 50 55 60
 Ile Cys Val Arg Lys Asn Leu Arg Glu Val Pro Asp Gly Ile Ser
 65 70 75
 Thr Asn Thr Arg Leu Leu Asn Leu His Glu Asn Gln Ile Gln Ile
 80 85 90
 Ile Lys Val Asn Ser Phe Lys His Leu Arg His Leu Glu Ile Leu
 95 100 105
 Gln Leu Ser Arg Asn His Ile Arg Thr Ile Glu Ile Gly Ala Phe
 110 115 120
 Asn Gly Leu Ala Asn Leu Asn Thr Leu Glu Leu Phe Asp Asn Arg
 125 130 135
 Leu Thr Thr Ile Pro Asn Gly Ala Phe Val Tyr Leu Ser Lys Leu
 140 145 150
 Lys Glu Leu Trp Leu Arg Asn Asn Pro Ile Glu Ser Ile Pro Ser
 155 160 165

Tyr	Ala	Phe	Asn	Arg	Ile	Pro	Ser	Leu	Arg	Arg	Leu	Asp	Leu	Gly	170	175	180
Glu	Leu	Lys	Arg	Leu	Ser	Tyr	Ile	Ser	Glu	Gly	Ala	Phe	Glu	Gly	185	190	195
Leu	Ser	Asn	Leu	Arg	Tyr	Leu	Asn	Leu	Ala	Met	Cys	Asn	Leu	Arg	200	205	210
Glu	Ile	Pro	Asn	Leu	Thr	Pro	Leu	Ile	Lys	Leu	Asp	Glu	Leu	Asp	215	220	225
Leu	Ser	Gly	Asn	His	Leu	Ser	Ala	Ile	Arg	Pro	Gly	Ser	Phe	Gln	230	235	240
Gly	Leu	Met	His	Leu	Gln	Lys	Leu	Trp	Met	Ile	Gln	Ser	Gln	Ile	245	250	255
Gln	Val	Ile	Glu	Arg	Asn	Ala	Phe	Asp	Asn	Leu	Gln	Ser	Leu	Val	260	265	270
Glu	Ile	Asn	Leu	Ala	His	Asn	Asn	Leu	Thr	Leu	Leu	Pro	His	Asp	275	280	285
Leu	Phe	Thr	Pro	Leu	His	His	Leu	Glu	Arg	Ile	His	Leu	His	His	290	295	300
Asn	Pro	Trp	Asn	Cys	Asn	Cys	Asp	Ile	Leu	Trp	Leu	Ser	Trp	Trp	305	310	315
Ile	Lys	Asp	Met	Ala	Pro	Ser	Asn	Thr	Ala	Cys	Cys	Ala	Arg	Cys	320	325	330
Asn	Thr	Pro	Pro	Asn	Leu	Lys	Gly	Arg	Tyr	Ile	Gly	Glu	Leu	Asp	335	340	345
Gln	Asn	Tyr	Phe	Thr	Cys	Tyr	Ala	Pro	Val	Ile	Val	Glu	Pro	Pro	350	355	360
Ala	Asp	Leu	Asn	Val	Thr	Glu	Gly	Met	Ala	Ala	Glu	Leu	Lys	Cys	365	370	375
Arg	Ala	Ser	Thr	Ser	Leu	Thr	Ser	Val	Ser	Trp	Ile	Thr	Pro	Asn	380	385	390
Gly	Thr	Val	Met	Thr	His	Gly	Ala	Tyr	Lys	Val	Arg	Ile	Ala	Val	395	400	405
Leu	Ser	Asp	Gly	Thr	Leu	Asn	Phe	Thr	Asn	Val	Thr	Val	Gln	Asp	410	415	420
Thr	Gly	Met	Tyr	Thr	Cys	Met	Val	Ser	Asn	Ser	Val	Gly	Asn	Thr	425	430	435
Thr	Ala	Ser	Ala	Thr	Leu	Asn	Val	Thr	Ala	Ala	Thr	Thr	Thr	Pro	440	445	450
Phe	Ser	Tyr	Phe	Ser	Thr	Val	Thr	Val	Glu	Thr	Met	Glu	Pro	Ser	455	460	465
Gln	Asp	Glu	Ala	Arg	Thr	Thr	Asp	Asn	Asn	Val	Gly	Pro	Thr	Pro	470	475	480

Val	Val	Asp	Trp	Glu	Thr	Thr	Asn	Val	Thr	Thr	Ser	Leu	Thr	Pro
				485					490					495
Gln	Ser	Thr	Arg	Ser	Thr	Glu	Lys	Thr	Phe	Thr	Ile	Pro	Val	Thr
				500					505					510
Asp	Ile	Asn	Ser	Gly	Ile	Pro	Gly	Ile	Asp	Glu	Val	Met	Lys	Thr
				515					520					525
Thr	Lys	Ile	Ile	Ile	Gly	Cys	Phe	Val	Ala	Ile	Thr	Leu	Met	Ala
				530					535					540
Ala	Val	Met	Leu	Val	Ile	Phe	Tyr	Lys	Met	Arg	Lys	Gln	His	His
				545					550					555
Arg	Gln	Asn	His	His	Ala	Pro	Thr	Arg	Thr	Val	Glu	Ile	Ile	Asn
				560					565					570
Val	Asp	Asp	Glu	Ile	Thr	Gly	Asp	Thr	Pro	Met	Glu	Ser	His	Leu
				575					580					585
Pro	Met	Pro	Ala	Ile	Glu	His	Glu	His	Leu	Asn	His	Tyr	Asn	Ser
				590					595					600
Tyr	Lys	Ser	Pro	Phe	Asn	His	Thr	Thr	Thr	Val	Asn	Thr	Ile	Asn
				605					610					615
Ser	Ile	His	Ser	Ser	Val	His	Glu	Pro	Leu	Leu	Ile	Arg	Met	Asn
				620					625					630
Ser	Lys	Asp	Asn	Val	Gln	Glu	Thr	Gln	Ile					
				635					640					

<210> 502
 <211> 2458
 <212> DNA
 <213> Homo Sapien

<400> 502
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 ccagctcgcc cgaggtccgt cggaggcgcc cggccgcccc ggagccaagc 150
 agcaactgag cggggaagcg cccgcgtccg gggatcgga tgtccctcct 200
 ccttctcctc ttgctagttt cctactatgt tggaaccttg gggactcaca 250
 ctgagatcaa gagagtggca gaggaaaagg tcactttgcc ctgccaccat 300
 caactggggc ttccagaaaa agacactctg gatattgaat ggctgctcac 350
 cgataatgaa ggggaacaaa aagtggatgat cacttactcc agtcgtcatg 400
 tctacaataa cttgactgag gaacagaagg gccgagtggc ctttgcttcc 450
 aatttctctg caggagatgc ctcttgagc attgaacctc tgaagcccag 500
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 ggagccatgt catcttaaaa gtcttagtga gaccatccaa gcccaagtgt 600

gagttggaag gagagctgac agaaggaagt gacctgactt tgcagtgtga 650
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 agaaagaggg agaggatgaa cgtctgcctc ccaaactag gattgactac 750
 aaccaccctg gacgagttct gctgcagaat cttaccatgt cctactctgg 800
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 ccagaggtga gaggttctga accaaagaaa gtccaccatg ctaatctgac 1250
 caaagcagaa accacacca gcatgatccc cagccagagc agagccttcc 1300
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 ggggtctttgg actcttctcg tcattggagc tcaagtcacc agccacacaa 1400
 ccagatgaga ggtcatctaa gtagcagtga gcattgcacg gaacagattc 1450
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 ctgacttaac ttcatttgtc ataaggtttg gatattaatt tcaaggggag 1900
 ttgaaatagt gggagatgga gaagagtga tgagtttctc ccactctata 1950
 ctaatctcac tatttgtatt gagccaaaaa taactatgaa aggagacaaa 2000
 aatttgtgac aaaggattgt gaagagcttt ccacttcat gatgttatga 2050
 ggattgttga caaacattag aaatatataa tggagcaatt gtggatttcc 2100
 cctcaaatca gatgcctcta aggactttcc tgctagatat ttctggaagg 2150
 agaaaataca acatgtcatt tatcaacgct cttagaaaga attcttctag 2200

Gln Tyr Val Gln Ser Ile Gly Met Val Ala Gly Ala Val Thr Gly
230 235 240

Ile Val Ala Gly Ala Leu Leu Ile Phe Leu Leu Val Trp Leu Leu
245 250 255

Ile Arg Arg Lys Asp Lys Glu Arg Tyr Glu Glu Glu Glu Arg Pro
260 265 270

Asn Glu Ile Arg Glu Asp Ala Glu Ala Pro Lys Ala Arg Leu Val
275 280 285

Lys Pro Ser Ser Ser Ser Ser Gly Ser Arg Ser Ser Arg Ser Gly
290 295 300

Ser Ser Ser Thr Arg Ser Thr Ala Asn Ser Ala Ser Arg Ser Gln
305 310 315

Arg Thr Leu Ser Thr Asp Ala Ala Pro Gln Pro Gly Leu Ala Thr
320 325 330

Gln Ala Tyr Ser Leu Val Gly Pro Glu Val Arg Gly Ser Glu Pro
335 340 345

Lys Lys Val His His Ala Asn Leu Thr Lys Ala Glu Thr Thr Pro
350 355 360

Ser Met Ile Pro Ser Gln Ser Arg Ala Phe Gln Thr Val
365 370

<210> 504
<211> 3060
<212> DNA
<213> Homo Sapien

<400> 504
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ctcctgtgcg gagtagtgga tttcgccaga agtttgagta tcactactcc 150
tgaagagatg attgaaaaag ccaaagggga aactgcctat ctgccatgca 200
aatttacgct tagtcccga gaccaggagc cgctggacat cgagtggctg 250
atatcaccag ctgataatca gaaggtggat caagtgatta ttttatattc 300
tggagacaaa atttatgatg actactatcc agatctgaaa ggccgagtac 350
attttacgag taatgatctc aaatctggtg atgcatcaat aaatgtaacg 400
aatttacaac tgtcagatat tggcacatat cagtgcagag tgaaaaaagc 450
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caggtgagag atgttacgtt gatggatctg aagaaattgg aagtgacttt 550
aagataaaat gtgaacaaaa agaaggttca cttccattac agtatgagtg 600
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tgacttcacg tggtatatct gtaaaaaatg cctctttctga gtactctggg 700

acatacagct gtacagtcag aaacagagtg ggctctgac agtgcctgtt 750
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 acccttaciaa gactgatgga attacagttg tataaatatg gactactgaa 1150
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 cttaaagtgt ttttaaaaaa agcacaaggc acagagatta gagcagctgt 1250
 aagaacacat ctactttatg caatggcatt agacatgtaa gtcagatgtc 1300
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 taacaaatth ttaacttttc atatgcatat tctgatatgt ggtcttttag 1450
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 acaaaccttc atgtgtatcc ctaaaccctaa aataaaaagt aaaaaaaaaa 2950
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 aaaaaaaaaa 3060

<210> 505
 <211> 352
 <212> PRT
 <213> Homo Sapien

<400> 505
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 Phe Ala Arg Ser Leu Ser Ile Thr Thr Pro Glu Glu Met Ile Glu
 20 25 30
 Lys Ala Lys Gly Glu Thr Ala Tyr Leu Pro Cys Lys Phe Thr Leu
 35 40 45
 Ser Pro Glu Asp Gln Gly Pro Leu Asp Ile Glu Trp Leu Ile Ser
 50 55 60
 Pro Ala Asp Asn Gln Lys Val Asp Gln Val Ile Ile Leu Tyr Ser
 65 70 75
 Gly Asp Lys Ile Tyr Asp Asp Tyr Tyr Pro Asp Leu Lys Gly Arg
 80 85 90
 Val His Phe Thr Ser Asn Asp Leu Lys Ser Gly Asp Ala Ser Ile
 95 100 105
 Asn Val Thr Asn Leu Gln Leu Ser Asp Ile Gly Thr Tyr Gln Cys
 110 115 120
 Lys Val Lys Lys Ala Pro Gly Val Ala Asn Lys Lys Ile His Leu

	125		130		135
Val Val Leu Val	Lys Pro Ser Gly Ala	Arg Cys Tyr Val Asp Gly			
	140	145			150
Ser Glu Glu Ile	Gly Ser Asp Phe Lys	Ile Lys Cys Glu Pro Lys			
	155	160			165
Glu Gly Ser Leu	Pro Leu Gln Tyr Glu	Trp Gln Lys Leu Ser Asp			
	170	175			180
Ser Gln Lys Met	Pro Thr Ser Trp Leu	Ala Glu Met Thr Ser Ser			
	185	190			195
Val Ile Ser Val	Lys Asn Ala Ser Ser	Glu Tyr Ser Gly Thr Tyr			
	200	205			210
Ser Cys Thr Val	Arg Asn Arg Val Gly	Ser Asp Gln Cys Leu Leu			
	215	220			225
Arg Leu Asn Val	Val Pro Pro Ser Asn	Lys Ala Gly Leu Ile Ala			
	230	235			240
Gly Ala Ile Ile	Gly Thr Leu Leu Ala	Leu Ala Leu Ile Gly Leu			
	245	250			255
Ile Ile Phe Cys	Cys Arg Lys Lys Arg	Arg Glu Glu Lys Tyr Glu			
	260	265			270
Lys Glu Val His	His Asp Ile Arg Glu	Asp Val Pro Pro Pro Lys			
	275	280			285
Ser Arg Thr Ser	Thr Ala Arg Ser Tyr	Ile Gly Ser Asn His Ser			
	290	295			300
Ser Leu Gly Ser	Met Ser Pro Ser Asn	Met Glu Gly Tyr Ser Lys			
	305	310			315
Thr Gln Tyr Asn	Gln Val Pro Ser Glu	Asp Phe Glu Arg Thr Pro			
	320	325			330
Gln Ser Pro Thr	Leu Pro Pro Ala Lys	Phe Lys Tyr Pro Tyr Lys			
	335	340			345
Thr Asp Gly Ile	Thr Val Val				
	350				

<210> 506
 <211> 1705
 <212> DNA
 <213> Homo Sapien

<400> 506
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 ccagctgcct ccaggcagcc agccctcaag catcacttac aggaccagag 150
 ggacaagaca tgactgtgat gaggagctgc ttctcgccaat ttaacaccaa 200
 gaagaattga ggctgcttgg gaggaaggcc aggaggaaca cgagactgag 250

agatgaattt tcaacagagg ctgcaaagcc tgtggacttt agccagaccc 300
 ttctgccctc ctttgctggc gacagcctct caaatgcaga tggttgtgct 350
 cccttgccctg ggttttaccc tgcttctctg gagccaggta tcagggggccc 400
 agggccaaga attccacttt gggccctgcc aagtgaaggg ggttggtccc 450
 cagaaactgt ggggaagcctt ctgggctgtg aaagacacta tgcaagctca 500
 ggataacatc acgagtggcc ggctgctgca gcaggagggt ctgcagaacg 550
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 ttgaaaactg ttttcaaaaa ccaccacaat agaacagttg aagtcaggac 650
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 tggccagctc accccatcat ccctttccct tggtgccctc cttttttttt 1550
 tatctagtc attcttccct aatcttccac ttgagtgtca agctgacctt 1600
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 ccctgctaataaaaagacaac ataactccaa aaaaaaaaaa aaaaaaaaaa 1700
 aaaaa 1705

<210> 507
 <211> 206
 <212> PRT

<213> Homo Sapien

<400> 507

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20 25 30
Val Val Leu Pro Cys Leu Gly Phe Thr Leu Leu Leu Trp Ser Gln
35 40 45
Val Ser Gly Ala Gln Gly Gln Glu Phe His Phe Gly Pro Cys Gln
50 55 60
Val Lys Gly Val Val Pro Gln Lys Leu Trp Glu Ala Phe Trp Ala
65 70 75
Val Lys Asp Thr Met Gln Ala Gln Asp Asn Ile Thr Ser Ala Arg
80 85 90
Leu Leu Gln Gln Glu Val Leu Gln Asn Val Ser Asp Ala Glu Ser
95 100 105
Cys Tyr Leu Val His Thr Leu Leu Glu Phe Tyr Leu Lys Thr Val
110 115 120
Phe Lys Asn His His Asn Arg Thr Val Glu Val Arg Thr Leu Lys
125 130 135
Ser Phe Ser Thr Leu Ala Asn Asn Phe Val Leu Ile Val Ser Gln
140 145 150
Leu Gln Pro Ser Gln Glu Asn Glu Met Phe Ser Ile Arg Asp Ser
155 160 165
Ala His Arg Arg Phe Leu Leu Phe Arg Arg Ala Phe Lys Gln Leu
170 175 180
Asp Val Glu Ala Ala Leu Thr Lys Ala Leu Gly Glu Val Asp Ile
185 190 195
Leu Leu Thr Trp Met Gln Lys Phe Tyr Lys Leu
200 205

<210> 508

<211> 924

<212> DNA

<213> Homo Sapien

<400> 508

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cggctctcagg agatgtctga tttccacaga catgcaccat atagaagaga 150
gtttccaaga aatcaaaaaga gccatccaag ctaaggacac cttcccaa 200
gtcactatcc tgtccacatt ggagactctg cagatcatta agcccttaga 250
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<210> 509

<211> 177

<212> PRT

<213> Homo Sapien

<400> 509

Met	Lys	Leu	Gln	Cys	Val	Ser	Leu	Trp	Leu	Leu	Gly	Thr	Ile	Leu	1	5	10	15
Ile	Leu	Cys	Ser	Val	Asp	Asn	His	Gly	Leu	Arg	Arg	Cys	Leu	Ile	20	25	30	
Ser	Thr	Asp	Met	His	His	Ile	Glu	Glu	Ser	Phe	Gln	Glu	Ile	Lys	35	40	45	
Arg	Ala	Ile	Gln	Ala	Lys	Asp	Thr	Phe	Pro	Asn	Val	Thr	Ile	Leu	50	55	60	
Ser	Thr	Leu	Glu	Thr	Leu	Gln	Ile	Ile	Lys	Pro	Leu	Asp	Val	Cys	65	70	75	
Cys	Val	Thr	Lys	Asn	Leu	Leu	Ala	Phe	Tyr	Val	Asp	Arg	Val	Phe	80	85	90	
Lys	Asp	His	Gln	Glu	Pro	Asn	Pro	Lys	Ile	Leu	Arg	Lys	Ile	Ser	95	100	105	
Ser	Ile	Ala	Asn	Ser	Phe	Leu	Tyr	Met	Gln	Lys	Thr	Leu	Arg	Gln	110	115	120	
Cys	Gln	Glu	Gln	Arg	Gln	Cys	His	Cys	Arg	Gln	Glu	Ala	Thr	Asn	125	130	135	
Ala	Thr	Arg	Val	Ile	His	Asp	Asn	Tyr	Asp	Gln	Leu	Glu	Val	His	140	145	150	
Ala	Ala	Ala	Ile	Lys	Ser	Leu	Gly	Glu	Leu	Asp	Val	Phe	Leu	Ala				

155

160

165

Trp Ile Asn Lys Asn His Glu Val Met Phe Ser Ala
170 175

<210> 510
<211> 996
<212> DNA
<213> Homo Sapien

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tccacaggtg tccactccca ggtccaactg cacctcgggt ctatcgataa 200
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ccacctgtac acagccacag ccaggaacag ctaccacctg cagatccaca 400
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ggogaagaga gccttcctgc caggcatgaa cccacccccg tactcccagt 700
tcctgtcccg gaggaacgag atccccctaa ttcacttcaa ccccccata 750
ccacggcggc acacccggag cgccgaggac gactcggagc gggacccccct 800
gaacgtgctg aagccccggg cccggatgac cccggccccg gcctcctggt 850
cacaggagct cccgagcgcc gaggacaaca gcccgatggc cagtgaccca 900
ttaggggtgg tcaggggagg tcgagtgaac acgcacgctg ggggaacggg 950
cccggaaggc tgccgcccct tcgccaagtt catctagggt cgctgg 996

<210> 511
<211> 251
<212> PRT
<213> Homo Sapien

<400> 511
Met Leu Gly Ala Arg Leu Arg Leu Trp Val Cys Ala Leu Cys Ser
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Val Cys Ser Met Ser Val Leu Arg Ala Tyr Pro Asn Ala Ser Pro
20 25 30

Leu	Leu	Gly	Ser	Ser	Trp	Gly	Gly	Leu	Ile	His	Leu	Tyr	Thr	Ala	
				35					40					45	
Thr	Ala	Arg	Asn	Ser	Tyr	His	Leu	Gln	Ile	His	Lys	Asn	Gly	His	
				50					55					60	
Val	Asp	Gly	Ala	Pro	His	Gln	Thr	Ile	Tyr	Ser	Ala	Leu	Met	Ile	
				65					70					75	
Arg	Ser	Glu	Asp	Ala	Gly	Phe	Val	Val	Ile	Thr	Gly	Val	Met	Ser	
				80					85					90	
Arg	Arg	Tyr	Leu	Cys	Met	Asp	Phe	Arg	Gly	Asn	Ile	Phe	Gly	Ser	
				95					100					105	
His	Tyr	Phe	Asp	Pro	Glu	Asn	Cys	Arg	Phe	Gln	His	Gln	Thr	Leu	
				110					115					120	
Glu	Asn	Gly	Tyr	Asp	Val	Tyr	His	Ser	Pro	Gln	Tyr	His	Phe	Leu	
				125					130					135	
Val	Ser	Leu	Gly	Arg	Ala	Lys	Arg	Ala	Phe	Leu	Pro	Gly	Met	Asn	
				140					145					150	
Pro	Pro	Pro	Tyr	Ser	Gln	Phe	Leu	Ser	Arg	Arg	Asn	Glu	Ile	Pro	
				155					160					165	
Leu	Ile	His	Phe	Asn	Thr	Pro	Ile	Pro	Arg	Arg	His	Thr	Arg	Ser	
				170					175					180	
Ala	Glu	Asp	Asp	Ser	Glu	Arg	Asp	Pro	Leu	Asn	Val	Leu	Lys	Pro	
				185					190					195	
Arg	Ala	Arg	Met	Thr	Pro	Ala	Pro	Ala	Ser	Cys	Ser	Gln	Glu	Leu	
				200					205					210	
Pro	Ser	Ala	Glu	Asp	Asn	Ser	Pro	Met	Ala	Ser	Asp	Pro	Leu	Gly	
				215					220					225	
Val	Val	Arg	Gly	Gly	Arg	Val	Asn	Thr	His	Ala	Gly	Gly	Thr	Gly	
				230					235					240	
Pro	Glu	Gly	Cys	Arg	Pro	Phe	Ala	Lys	Phe	Ile					
				245					250						

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 <211> 2015
 <212> DNA
 <213> Homo Sapien

<400> 512
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 gagcagacac tgcatgaca acggacgaca cagaagtgcc cgctatgact 200
 ctagcaccgg gccacgccgc tctggaaact caaacgctga gcgctgagac 250
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 caggcagtga tcccaggagaa gccatctttg acaccctttg caccgatgac 500
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 cacctccaca gaagctaagg gcctgtcctc agagagcagt gcctcttccg 600
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 cagcgctct tccgacggcc cccatccagt catcaccccg tcatggtccc 750
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 caccacagag tcagctgcac ctcatgccac ggttgggacc ccactcccca 1050
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 agtgagctc tggtcacagt tagcaggaat cccctggaag aaacctcagc 1150
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 agctctgctt cctcctacag cccctcggaa gccgccctca agaacttcac 1300
 cccttcagag acaccgacca tggacatgc aaccaagggg cccttcccca 1350
 ccagcaggg a ccctcttct tctgtccctc cgactacaac caacagcagc 1400
 cgagggacga acagcacctt agccaagatc acaacctcag cgaagaccac 1450
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 gggcagcatg tccaagcccc taaccccaga tgtggcaaca ggaccctcgc 1850
 tcacatccac cggagtgtat gtatggggag gggcttcacc tggtcccaga 1900

gggtgtccttg gactcacctt ggcacatggt ctgtgtttca gtaaagagag 1950
acctgatcac ccatctgtgt gcttccatcc tgcattaaaa ttactcagt 2000
gtggcccaaa aaaaa 2015

<210> 513
<211> 482
<212> PRT
<213> Homo Sapien

<400> 513
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Trp Glu Val Gly Val Ser Gly Ser Ser Ala Gly Pro Ser Thr Arg
20 25 30
Arg Ala Asp Thr Ala Met Thr Thr Asp Asp Thr Glu Val Pro Ala
35 40 45
Met Thr Leu Ala Pro Gly His Ala Ala Leu Glu Thr Gln Thr Leu
50 55 60
Ser Ala Glu Thr Ser Ser Arg Ala Ser Thr Pro Ala Gly Pro Ile
65 70 75
Pro Glu Ala Glu Thr Arg Gly Ala Lys Arg Ile Ser Pro Ala Arg
80 85 90
Glu Thr Arg Ser Phe Thr Lys Thr Ser Pro Asn Phe Met Val Leu
95 100 105
Ile Ala Thr Ser Val Glu Thr Ser Ala Ala Ser Gly Ser Pro Glu
110 115 120
Gly Ala Gly Met Thr Thr Val Gln Thr Ile Thr Gly Ser Asp Pro
125 130 135
Glu Glu Ala Ile Phe Asp Thr Leu Cys Thr Asp Asp Ser Ser Glu
140 145 150
Glu Ala Lys Thr Leu Thr Met Asp Ile Leu Thr Leu Ala His Thr
155 160 165
Ser Thr Glu Ala Lys Gly Leu Ser Ser Glu Ser Ser Ala Ser Ser
170 175 180
Asp Gly Pro His Pro Val Ile Thr Pro Ser Arg Ala Ser Glu Ser
185 190 195
Ser Ala Ser Ser Asp Gly Pro His Pro Val Ile Thr Pro Ser Arg
200 205 210
Ala Ser Glu Ser Ser Ala Ser Ser Asp Gly Pro His Pro Val Ile
215 220 225
Thr Pro Ser Trp Ser Pro Gly Ser Asp Val Thr Leu Leu Ala Glu
230 235 240
Ala Leu Val Thr Val Thr Asn Ile Glu Val Ile Asn Cys Ser Ile
245 250 255

Thr	Glu	Ile	Glu	Thr	Thr	Thr	Ser	Ser	Ile	Pro	Gly	Ala	Ser	Asp	260	265	270
Ile	Asp	Leu	Ile	Pro	Thr	Glu	Gly	Val	Lys	Ala	Ser	Ser	Thr	Ser	275	280	285
Asp	Pro	Pro	Ala	Leu	Pro	Asp	Ser	Thr	Glu	Ala	Lys	Pro	His	Ile	290	295	300
Thr	Glu	Val	Thr	Ala	Ser	Ala	Glu	Thr	Leu	Ser	Thr	Ala	Gly	Thr	305	310	315
Thr	Glu	Ser	Ala	Ala	Pro	His	Ala	Thr	Val	Gly	Thr	Pro	Leu	Pro	320	325	330
Thr	Asn	Ser	Ala	Thr	Glu	Arg	Glu	Val	Thr	Ala	Pro	Gly	Ala	Thr	335	340	345
Thr	Leu	Ser	Gly	Ala	Leu	Val	Thr	Val	Ser	Arg	Asn	Pro	Leu	Glu	350	355	360
Glu	Thr	Ser	Ala	Leu	Ser	Val	Glu	Thr	Pro	Ser	Tyr	Val	Lys	Val	365	370	375
Ser	Gly	Ala	Ala	Pro	Val	Ser	Ile	Glu	Ala	Gly	Ser	Ala	Val	Gly	380	385	390
Lys	Thr	Thr	Ser	Phe	Ala	Gly	Ser	Ser	Ala	Ser	Ser	Tyr	Ser	Pro	395	400	405
Ser	Glu	Ala	Ala	Leu	Lys	Asn	Phe	Thr	Pro	Ser	Glu	Thr	Pro	Thr	410	415	420
Met	Asp	Ile	Ala	Thr	Lys	Gly	Pro	Phe	Pro	Thr	Ser	Arg	Asp	Pro	425	430	435
Leu	Pro	Ser	Val	Pro	Pro	Thr	Thr	Thr	Asn	Ser	Ser	Arg	Gly	Thr	440	445	450
Asn	Ser	Thr	Leu	Ala	Lys	Ile	Thr	Thr	Ser	Ala	Lys	Thr	Thr	Met	455	460	465
Lys	Pro	Gln	Gln	Pro	Arg	Pro	Arg	Leu	Pro	Gly	Arg	Gly	Arg	Pro	470	475	480

Gln Thr

<210> 514
 <211> 2284
 <212> DNA
 <213> Homo Sapien

<400> 514
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 ggcgcggggg tcctctcgac gccagagaga aatctcatca tctgtgcagc 150
 cttcttaaag caaactaaga ccagagggag gattatcctt gacctttgaa 200
 gacccaaaact aaactgaaat ttaaaatgtt cttcggggga gaaggagct 250

tgacttacac tttggaata atttgcttcc tgacactaag gctgtctgct 300
 agtcagaatt gcctcaaaaa gagtctagaa gatgttgtca ttgacatcca 350
 gtcattctctt tctaagggaa tcagaggcaa tgagcccgta tatacttcaa 400
 ctcaagaaga ctgcattaat tcttgctggt caacaaaaaa catatcaggg 450
 gacaaagcat gtaacttgat gatcttcgac actcgaaaaa cagctagaca 500
 acccaactgc tacctatttt tctgtcccaa cgaggaagcc tgtccattga 550
 aaccagcaaa aggacttatg agttacagga taattacaga ttttccatct 600
 ttgaccagaa atttgccaag ccaagagtta cccaggaag attctctctt 650
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 tgggtgcctg ttctgggtga taggcctgt cctcctgggt agaatcctt 1450
 cggaatcact ccgcaggaaa cgttactcaa gactggatta tttgatcaat 1500
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 acacctgggt gatTTTTTgta ttttagtag agacggggtt tcacatggt 1850

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 attttgggta atctgtctct aaaatattag ctaaaaacaa agctctatgt 2050
 aaagtaataa agtataattg ccatataaat ttcaaaattc aactggcttt 2100
 tatgcaaaga aacagggttag gacatctagg ttccaattca ttcacattct 2150
 tggttccaga taaaatcaac tgtttatatc aatttctaataa ggatttgctt 2200
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 aattaaatat ttgaataaat cttttgttac tcaa 2284

<210> 515
 <211> 431
 <212> PRT
 <213> Homo Sapien

<400> 515
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 Lys Lys Ser Leu Glu Asp Val Val Ile Asp Ile Gln Ser Ser Leu
 35 40 45
 Ser Lys Gly Ile Arg Gly Asn Glu Pro Val Tyr Thr Ser Thr Gln
 50 55 60
 Glu Asp Cys Ile Asn Ser Cys Cys Ser Thr Lys Asn Ile Ser Gly
 65 70 75
 Asp Lys Ala Cys Asn Leu Met Ile Phe Asp Thr Arg Lys Thr Ala
 80 85 90
 Arg Gln Pro Asn Cys Tyr Leu Phe Phe Cys Pro Asn Glu Glu Ala
 95 100 105
 Cys Pro Leu Lys Pro Ala Lys Gly Leu Met Ser Tyr Arg Ile Ile
 110 115 120
 Thr Asp Phe Pro Ser Leu Thr Arg Asn Leu Pro Ser Gln Glu Leu
 125 130 135
 Pro Gln Glu Asp Ser Leu Leu His Gly Gln Phe Ser Gln Ala Val
 140 145 150
 Thr Pro Leu Ala His His His Thr Asp Tyr Ser Lys Pro Thr Asp
 155 160 165
 Ile Ser Trp Arg Asp Thr Leu Ser Gln Lys Phe Gly Ser Ser Asp
 170 175 180
 His Leu Glu Lys Leu Phe Lys Met Asp Glu Ala Ser Ala Gln Leu
 185 190 195

TOHTE" OH06660

Leu	Ala	Tyr	Lys	Glu	Lys	Gly	His	Ser	Gln	Ser	Ser	Gln	Phe	Ser
				200					205					210
Ser	Asp	Gln	Glu	Ile	Ala	His	Leu	Leu	Pro	Glu	Asn	Val	Ser	Ala
				215					220					225
Leu	Pro	Ala	Thr	Val	Ala	Val	Ala	Ser	Pro	His	Thr	Thr	Ser	Ala
				230					235					240
Thr	Pro	Lys	Pro	Ala	Thr	Leu	Leu	Pro	Thr	Asn	Ala	Ser	Val	Thr
				245					250					255
Pro	Ser	Gly	Thr	Ser	Gln	Pro	Gln	Leu	Ala	Thr	Thr	Ala	Pro	Pro
				260					265					270
Val	Thr	Thr	Val	Thr	Ser	Gln	Pro	Pro	Thr	Thr	Leu	Ile	Ser	Thr
				275					280					285
Val	Phe	Thr	Arg	Ala	Ala	Ala	Thr	Leu	Gln	Ala	Met	Ala	Thr	Thr
				290					295					300
Ala	Val	Leu	Thr	Thr	Thr	Phe	Gln	Ala	Pro	Thr	Asp	Ser	Lys	Gly
				305					310					315
Ser	Leu	Glu	Thr	Ile	Pro	Phe	Thr	Glu	Ile	Ser	Asn	Leu	Thr	Leu
				320					325					330
Asn	Thr	Gly	Asn	Val	Tyr	Asn	Pro	Thr	Ala	Leu	Ser	Met	Ser	Asn
				335					340					345
Val	Glu	Ser	Ser	Thr	Met	Asn	Lys	Thr	Ala	Ser	Trp	Glu	Gly	Arg
				350					355					360
Glu	Ala	Ser	Pro	Gly	Ser	Ser	Ser	Gln	Gly	Ser	Val	Pro	Glu	Asn
				365					370					375
Gln	Tyr	Gly	Leu	Pro	Phe	Glu	Lys	Trp	Leu	Leu	Ile	Gly	Ser	Leu
				380					385					390
Leu	Phe	Gly	Val	Leu	Phe	Leu	Val	Ile	Gly	Leu	Val	Leu	Leu	Gly
				395					400					405
Arg	Ile	Leu	Ser	Glu	Ser	Leu	Arg	Arg	Lys	Arg	Tyr	Ser	Arg	Leu
				410					415					420
Asp	Tyr	Leu	Ile	Asn	Gly	Ile	Tyr	Val	Asp	Ile				
				425					430					

<210> 516
 <211> 2749
 <212> DNA
 <213> Homo Sapien

<220>
 <221> unsure
 <222> 1869, 1887
 <223> unknown base

<400> 516
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gcgggttcga aggggacact gtgtccctgc agtgcaccta caggggaagag 150
ctgagggacc accggaagta ctggtgcagg aagggtggga tcctcttctc 200
tcgctgtctc ggcacatct atgcagaaga agaaggccag gagacaatga 250
agggcagggc gtccatccgt gacagccgcc aggagctctc gctcattgtg 300
accctgtgga acctcaccct gcaagacgct ggggagtact ggtgtggggc 350
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 tctttttaca gagcaattat cttgtatata caactttgta tctgccttt 2650
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 gaccttttta taaataaaat gttcatcagc tgcataaaaa aaaaaaaaaa 2749

<210> 517
 <211> 332
 <212> PRT
 <213> Homo Sapien

<400> 517
 Met Arg Leu Leu Val Leu Leu Trp Gly Cys Leu Leu Leu Pro Gly
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 Tyr Glu Ala Leu Glu Gly Pro Glu Glu Ile Ser Gly Phe Glu Gly
 20 25 30
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 35 40 45
 His Arg Lys Tyr Trp Cys Arg Lys Gly Gly Ile Leu Phe Ser Arg
 50 55 60
 Cys Ser Gly Thr Ile Tyr Ala Glu Glu Glu Gly Gln Glu Thr Met
 65 70 75

Lys	Gly	Arg	Val	Ser	Ile	Arg	Asp	Ser	Arg	Gln	Glu	Leu	Ser	Leu	80	85	90
Ile	Val	Thr	Leu	Trp	Asn	Leu	Thr	Leu	Gln	Asp	Ala	Gly	Glu	Tyr	95	100	105
Trp	Cys	Gly	Val	Glu	Lys	Arg	Gly	Pro	Asp	Glu	Ser	Leu	Leu	Ile	110	115	120
Ser	Leu	Phe	Val	Phe	Pro	Gly	Pro	Cys	Cys	Pro	Pro	Ser	Pro	Ser	125	130	135
Pro	Thr	Phe	Gln	Pro	Leu	Ala	Thr	Thr	Arg	Leu	Gln	Pro	Lys	Ala	140	145	150
Lys	Ala	Gln	Gln	Thr	Gln	Pro	Pro	Gly	Leu	Thr	Ser	Pro	Gly	Leu	155	160	165
Tyr	Pro	Ala	Ala	Thr	Thr	Ala	Lys	Gln	Gly	Lys	Thr	Gly	Ala	Glu	170	175	180
Ala	Pro	Pro	Leu	Pro	Gly	Thr	Ser	Gln	Tyr	Gly	His	Glu	Arg	Thr	185	190	195
Ser	Gln	Tyr	Thr	Gly	Thr	Ser	Pro	His	Pro	Ala	Thr	Ser	Pro	Pro	200	205	210
Ala	Gly	Ser	Ser	Arg	Pro	Pro	Met	Gln	Leu	Asp	Ser	Thr	Ser	Ala	215	220	225
Glu	Asp	Thr	Ser	Pro	Ala	Leu	Ser	Ser	Gly	Ser	Ser	Lys	Pro	Arg	230	235	240
Val	Ser	Ile	Pro	Met	Val	Arg	Ile	Ile	Ala	Pro	Val	Leu	Val	Leu	245	250	255
Leu	Ser	Leu	Leu	Ser	Ala	Ala	Gly	Leu	Ile	Ala	Phe	Cys	Ser	His	260	265	270
Leu	Leu	Leu	Trp	Arg	Lys	Glu	Ala	Gln	Gln	Ala	Thr	Glu	Thr	Gln	275	280	285
Arg	Asn	Glu	Lys	Phe	Trp	Leu	Ser	Arg	Leu	Thr	Ala	Glu	Glu	Lys	290	295	300
Glu	Ala	Pro	Ser	Gln	Ala	Pro	Glu	Gly	Asp	Val	Ile	Ser	Met	Pro	305	310	315
Pro	Leu	His	Thr	Ser	Glu	Glu	Glu	Leu	Gly	Phe	Ser	Lys	Phe	Val	320	325	330

Ser Ala

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gaagcaagtg cccagctc 18

<210> 530

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Variable	Mean	SD	Min	Max
Age	34.5	10.2	22	55
Gender	0.5	0.5	0	1
Marital status	0.6	0.5	0	1
Education	12.5	1.5	10	15
Income	1500	500	1000	2500
Health status	0.8	0.2	0	1
Employment status	0.7	0.3	0	1
Family size	3.2	1.1	1	5
Home ownership	0.9	0.1	0	1
Auto ownership	0.8	0.2	0	1
Life satisfaction	4.5	1.2	1	7
Health satisfaction	5.2	1.0	1	7
Financial satisfaction	4.8	1.1	1	7
Relationship satisfaction	5.0	1.0	1	7
Community satisfaction	4.6	1.1	1	7
Overall life satisfaction	4.7	1.1	1	7

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cgggtcctg ctctttgg 18

<211> 24

<213> Artificial Sequence

<223> Synthetic oligonucleotide probe

caccgtagct gggagcgcac tcac 24

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